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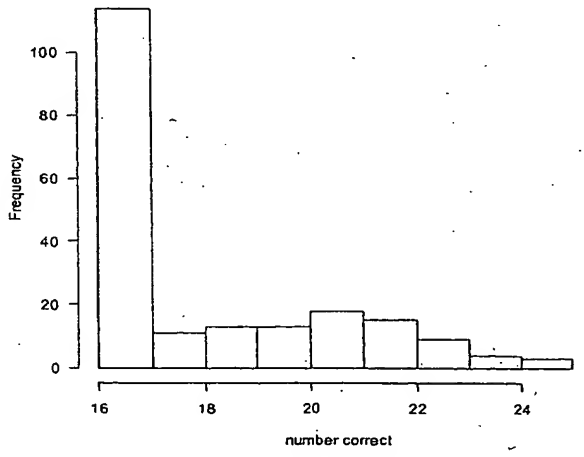

(57) Abstract: A method and apparatus is described for identifying a subset of components of a system, the subset being capable of predicting a feature of a test sample. The method comprises generating a linear combination of components and component weights in which values for each component are determined from data generated from a plurality of training samples, each training sample having a known feature. A model is defined for the probability distribution of a feature wherein the model is conditional on the linear combination and wherein the model is not a combination of a binomial distribution for a two class response with a probit function linking the linear combination and the expectation of the response. A prior distribution is constructed for the component weights of the linear combination comprising a hyperprior having a high probability density close to zero, and the prior distribution and the model are combined to generate a posterior distribution. A subset of components is identified having component weights that maximise the posterior distribution.

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METHOD AND APPARATUS FOR IDENTIFYING DIAGNOSTIC COMPONENTS OF A SYSTEM

FIELD OF THE INVENTION

The present invention relates to a method and apparatus for identifying components of a system from data generated from samples from the system, which components are capable of predicting a feature of the sample within the system and, particularly, but not exclusively, the present invention relates to a method and apparatus for identifying components of a biological system from data generated by a biological method, which components are capable of predicting a feature of interest associated with a sample from the biological system.

BACKGROUND OF THE INVENTION

There are any number of "systems" in existence which can be classified into different features of interest. The term "system" essentially includes all types of systems for which data can be provided, including chemical systems, financial systems (e.g. credit systems for individuals, groups or organisations, loan histories), geological systems, and many more. It is desirable to be able to utilise data generated from the systems (e.g. statistical data) to identify particular features of samples from the system (e.g. to assist with analysis of a financial system to identify the groups which exist in the financial system (e.g. in very simple terms those who have "good" credit and those who are a credit risk). Where there is a large amount of statistical data, the identification of components from that data which are predictive of a particular feature of a sample from the system is a difficult task, generally because there is a large amount of data to process, the majority of which may not provide any indication or little indication of the features of interest of a particular sample from which the data is taken. In addition, components that are

identified using training sample data are often ineffective at identifying features on test samples data when the test sample data has a high degree of variability relative to the training sample data. This is often the case in situations when, for example, data is obtained from many different sources, as it is often impossible to control the conditions under which the data is collected from each individual source.

An example of a type of system where these problems are particularly pertinent, is a biological system and the following description refers specifically to biological systems. The present invention is not limited to use with biological systems, however, and it has general application to any system.

Recent advances in biotechnology have resulted in the development of biological methods for large scale screening of systems and analysis of samples. Such methods include, for example, DNA, RNA or antibody microarray analysis, proteomics analysis, proteomics electrophoresis gel analysis and high throughput screening techniques. These types of methods often result in the generation of data that can have up to 30,000 or more components for each sample that is tested.

It is obviously important to be able to identify features of interest in samples from biological systems. For example, to classify groups such as "diseased" and "non-diseased". Many of these biological methods would be useful as diagnostic tools predicting features of a sample in the biological systems (e.g. for identifying diseases by screening tissues or body fluids, or as tools for determining, for example, the efficacy of pharmaceutical compounds).

Use of biological methods such as biotechnology arrays in such applications to date has been limited owing to the

large amount of data that is generated from these types of methods, and the lack of efficient methods for screening the data for meaningful results. Consequently, analysis of biological data using prior art methods either fails to make full use of the information inn the data, or is time consuming, prone to false positive and negative results and requires large amounts of computer memory if a meaningful result is to be obtained from the data. This is problematic in large scale screening scenarios where rapid and accurate screening is required.

There is therefore a need for an improved method, in particular for analysis of biological data, and, more generally, for an improved method of analysing data from any system in order to predict a feature of interest for a sample from the system.

SUMMARY OF THE INVENTION

In a first aspect, the invention provides a method for identifying a subset of components of a system, the subset being capable of predicting a feature of a test sample, the method comprising the steps of;

(a) generating a linear combination of components and component weights in which values for each component are determined from data generated from a plurality of training samples, each training sample having a known feature;

(b) defining a model for the probability distribution of a feature wherein the model is conditional on the linear combination and wherein the model is not a combination of a binomial distribution for a two class response with a probit function linking the linear combination and the expectation of the response ;

(c) constructing a prior distribution for the component weights of the linear combination comprising a hyperprior having a high probability density close

to zero;

(d) combining the prior distribution and the model to generate a posterior distribution;

(e) identifying a subset of components having component weights that maximise the posterior distribution.

The method utilises training samples having a known feature in order to identify a subset of components which can predict a feature for a training sample. Subsequently, knowledge of the subset of components can be used for tests, for example clinical tests, to predict a feature such as whether a tissue sample is malignant or benign, or what is the weight of a tumour, or provide an estimated time for survival of a patient having a particular condition. As used herein, the term "feature" refers to any response or identifiable trait or character that is associated with a sample. For example, a feature may be a particular time to an event for a particular sample, or the size or quantity of a sample, or the class or group into which a sample can be classified.

The method of the present invention estimates the component weights utilising a Bayesian statistical method. Preferably, where there are a large amount of components generated from the system (which will usually be the case for the method of the present invention to be effective) the method preferably makes an a priori assumption that the majority of the components are unlikely to be components that will form part of the subset of components for predicting a feature. The assumption is therefore made that the majority of component weights are likely to be zero. A model is constructed which, with this assumption in mind, sets the component weights so that the posterior probability of the weights is maximised. Components having a weight below a pre-determined threshold (which will be the majority of them in accordance with the a priori

assumption) are dispensed with. The process is iterated until the remaining diagnostic components are identified. This method is quick, mainly because of the a priori assumption which results in rapid elimination of the majority of components.

Most features of a system typically exhibit a probability distribution, and the probability distribution of a feature can be modelled using statistical models which are based on the data generated from the training samples. The method of the invention utilises statistical models which model the probability distribution for a feature of interest or a series of features of interest. Thus, for a feature of interest having a particular probability distribution, an appropriate model is defined that models that distribution. The method may use any model that is conditional on the linear combination, and is preferably a mathematical equation in the form of a likelihood function that provides a probability distribution based on the data obtained from the training samples. Preferably, the likelihood function is based on a previously described model for describing some probability distribution. In one embodiment, the model is a likelihood function based on a model selected from the group consisting of a multinomial or binomial logistic regression, generalised linear model, Cox's proportional hazards model, accelerated failure model, parametric survival model, a chi-squared distribution model or an exponential distribution model.

In one embodiment, the likelihood function is based on a multinomial or binomial logistic regression. The binomial or multinomial logistic regression preferably models a feature having a multinomial or binomial distribution. A binomial distribution is a statistical distribution having two possible classes or groups such as an on/off state. Examples of such groups include

dead/alive, improved/not improved, depressed/not depressed. A multinomial distribution is a generalisation of the binomial distribution in which a plurality of classes or groups are possible for each of a plurality of samples, or in other words, a sample may be classified into one of a plurality of classes or groups. Thus, by defining a likelihood function based on a multinomial or binomial logistic regression, it is possible to identify subsets of components that are capable of classifying a sample into one of a plurality of pre-defined groups or classes. To do this, training samples are grouped into a plurality of sample groups (or "classes") based on a predetermined feature of the training samples in which the members of each sample group have a common feature and are assigned a common group identifier. A likelihood function is formulated based on a multinomial or binomial logistic regression conditional on the linear combination (which incorporates the data generated from the grouped training samples). The feature may be any desired classification by which the training samples are to be grouped. For example, the features for classifying tissue samples may be that the tissue is normal, malignant or benign; the feature for classifying cell samples may be that the cell is a leukemia cell or a healthy cell, that the training samples are obtained from the blood of patients having or not having a certain condition, or that the training samples are from a cell from one of several types of cancer as compared to a normal cell.

Preferably, the likelihood function based on the logistic regression is of the form:

$$L = \prod_{i=1}^{n} \left(\prod_{g=1}^{G-1} \left\{ \frac{e^{x_i^T \beta_g}}{\left(1 + \sum_{g=1}^{G-1} e^{x_i^T \beta_g}\right)} \right\}^{e_{ig}} \left\{ \frac{1}{1 + \sum_{h=1}^{G-1} e^{x_i^T \beta_h}} \right\}^{e_{iG}} \right)$$

wherein

$x_i^T \beta_g$ is a linear combination generated from input data from training sample i with component weights β_g;

x_i^T is the components for the i^{th} Row of X and β_g is a set of component weights for sample class g;

$e_{ig}=1$ if training sample i is a member of class g, $e_{ig}=0$ otherwise;

and

X is data from n training samples comprising p components.

In another embodiment, the likelihood function is based on an ordered categorical logistic regression. The ordered categorical logistic regression models a multinomial distribution in which the classes are in a particular order (ordered classes such as for example, classes of increasing or decreasing disease severity). By defining a likelihood function based on an ordered categorical logistic regression, it is possible to identify a subset of components that is capable of classifying a sample into a class wherein the class is one of a plurality of predefined ordered classes. By defining a series of group identifiers in which each group identifier corresponds to a member of an ordered class, and grouping the training samples into one of the ordered classes based on predetermined features of the training samples, a likelihood function can be formulated based on a categorical ordered logistic regression which is conditional on the linear combination (which incorporates the data generated from the grouped training samples).

Preferably, the likelihood function based on the

categorical ordered logistic regression is of the form:

$$L = \prod_{i=1}^{N} \prod_{k=1}^{G-1} \left(\frac{\gamma_{ik}}{\gamma_{ik+1}} \right)^{r_{ik}} \left(\frac{\gamma_{ik+1} - \gamma_{ik}}{\gamma_{ik+1}} \right)^{r_{ik+1} - r_{ik}}$$

$$\operatorname{logit}\left(\frac{\gamma_{ik+1} - \gamma_{ik}}{\gamma_{ik+1}} \right) = \operatorname{logit}\left(\frac{\pi_{ik}}{\gamma_{ik+1}} \right) = \theta_k + x_i^T \beta^*$$

Wherein

γ_{ik} is the probability that training sample i belongs to a class with identifier less than or equal to k (where the total of ordered classes is G);

$x_i^T \beta^*$ is a linear combination generated from input data from training sample i with component weights β^*;

x_i^T is the components for the i^{th} Row of X ;

r_{ij} is as defined as;

$$r_{ij} = \sum_{g=1}^{j} c_{ig}$$

where

$$c_{ij} = \begin{cases} 1, & \text{if observation i in class j} \\ 0, & \text{otherwise} \end{cases}$$

In another embodiment of the present invention, the likelihood function is based on a generalised linear model. The generalised linear model preferably models a feature which has a distribution belonging to the regular exponential family of distributions . Examples of regular exponential family distributions include normal distribution, Gaussian distribution, Poisson distribution, gamma distribution and inverse gamma

distribution. Thus, in another embodiment of the method of the invention, a subset of components is identified that is capable of predicting a predefined characteristic of a sample that lies within a regular exponential family of distributions by defining a generalised linear model which models the characteristic to be predicted. Examples of a characteristic that may be predicted using a generalised linear model include any quantity of a sample that exhibits the specified distribution such as, for example, the weight, size, counts, group membership or other dimensions or quantities or properties of a sample.

Preferably, the generalised linear model is of the form:

$$\log p(y \mid \beta, \varphi) = \sum_{i=1}^{N} \{ \frac{y_i \theta_i - b(\theta_i)}{a_i(\varphi)} + c(y_i, \varphi) \}$$

Wherein

$Y = (y_1, \ldots, y_n)^T$, and y_i is the characteristic measured on the i^{th} sample;

$a_i(\phi) = \phi / w_i$ with the w_i being a fixed set of known weights and ϕ a single scale parameter;

the functions b(.) and c(.)are preferably as defined by Nelder and Wedderburn (1972);

Preferably,

$$E\{y_i\} = b'(\theta_i)$$

$$Var\{y\} = b''(\theta_i) a_i(\varphi) = \tau_i^2 a_i(\varphi) \quad .$$

Preferably, each observation has a set of covariates x_i and a linear predictor $\eta_i = x_i^T \beta$. The relationship between the mean of the i^{th} observation and its linear predictor is preferably given by the link function $\eta_i = g(\mu_i) = g(b'(\theta_i))$. The inverse of the link is denoted by h, which is preferably:

$$E\{y_i\} = b'(\theta_i) = h(\eta_i) .$$

In another embodiment, the method of the present invention may be used to predict the time to an event for a sample by utilising a likelihood function based on a hazard model which preferably estimates the probability of a time to an event given that the event has not taken place at the time of obtaining the data. In one embodiment, the likelihood function is based on a model selected from the group consisting of Cox's proportional hazards model, parametric survival model and accelerated failure times model. Cox's proportional hazards model permits the time to an event to be modelled on a set of components and component weights without making restrictive assumptions about the form of the hazard function . The accelerated failure model is a general model for data consisting of survival times in which the component measurements are assumed to act multiplicatively on the time-scale, and so affect the rate at which an individual proceeds along the time axis. Thus, the accelerated survival model can be interpreted in terms of the speed of progression of, for example, disease. The parametric survival model is one in which the distribution function for the time to an event (eg survival time) is modelled by a known distribution or has a specified parametric formulation. Among the commonly used survival distributions are the Weibull, exponential and extreme value distributions.

Preferably, a subset of components capable of predicting the time to an event for a sample is identified by defining a likelihood based on Cox's proportional hazards model, a parametric survival model or an accelerated survival times model, which comprises measuring the time elapsed for a plurality of samples from the time the sample is obtained to the time of the event.

Preferably, the likelihood function for predicting the time to an event is of the form:

$$Log\ (Partial)\ Likelihood = \sum_{i=1}^{N} g_i\left(\underset{\sim}{\beta}, \underset{\sim}{\varphi}; X, \underset{\sim}{y}, \underset{\sim}{c}\right)$$

where $\underset{\sim}{\beta}^t = \left(\beta_1, \beta_2, \cdots, \beta_p\right)$ and $\underset{\sim}{\varphi}^t = \left(\varphi_1, \varphi_2, \cdots, \varphi_q\right)$ are the model parameters.

Preferably, the likelihood function based on Cox's proportional hazards model is of the form:

$$L\left(\underset{\sim}{t} \mid \underset{\sim}{\beta}\right) = \prod_{j=1}^{N}\left(\frac{exp\left(Z_j \underset{\sim}{\beta}\right)}{\sum_{i \in \Re_j} exp\left(Z_i \underset{\sim}{\beta}\right)}\right)^{d_j}$$

Where Z is preferably a matrix that is the re-arrangement of the rows of X where the ordering of the rows of Z corresponds to the ordering induced by the ordering of the survival times and d is the result of ordering the censoring index with the same permutation required to order survival times. Also Z_j is the j^{th} row of the matrix Z and d_j is the j^{th} element of d and where $\underset{\sim}{\beta}^T = \left(\beta_1, \beta_2, \cdots, \beta_p\right)$, and $\Re_j = \{i : i = j, j+1, \cdots, N\}$ = the risk set at the j^{th} ordered event time $t_{(j)}$.

Preferably the log likelihood function based on the Parametric Survival model is of the form:

$$log(L) = \sum_{i=1}^{N}\left\{c_i\, log\left(\mu_i\right) - \mu_i + c_i\left(log\left(\frac{\lambda(y_i)}{\Lambda\left(y_i; \underset{\sim}{\varphi}\right)}\right)\right)\right\}$$

where

$\mu_i = \Lambda\left(y_i; \underset{\sim}{\varphi}\right) exp\left(X_i \underset{\sim}{\beta}\right)$;

$c_i = 1$ if the i^{th} sample is uncensored and $c_i = 0$ if the i^{th}

sample is uncensored.
This form of the likelihood function is shared by the Weibull, exponential and extreme value distributions. The functions $\lambda(.)$ and $\Lambda(.)$ are as defined by Aitkin and Clayton (1980).

For any defined models, the component weights are typically estimated using a Bayesian statistical model (Kotz and Johnson, 1983) in which a posterior distribution of the component weights is formulated which combines the likelihood function and a prior distribution. The component weights are estimated by maximising the posterior distribution of the weights given the data generated for each training sample. Thus, the objective function to be maximised consists of the likelihood function based on a model for the feature as discussed above and a prior distribution for the weights.

Preferably, the prior distribution is of the form:

$$p(\beta)=\int_{v^2} p(\beta\,|v^2)\,p(v^2)\,dv^2$$

wherein v is a p x 1 vector of hyperparameters, and where $p(\beta\,|v^2)$ is $N(0,\mathrm{diag}\{v^2\})$ and $p(v^2)$ is some hyperprior distribution for v^2. This hyperprior distribution (which is preferably the same for all embodiments of the method) may be expressed using different notational conventions, and in the detailed description of the preferred embodiments (see below), the following notational conventions are adopted merely for convenience for the particular preferred embodiment:

As used herein, when the likelihood function for the probability distribution is based on a multinomial or binomial logistic regression, the notation for the prior distribution is:

$$P(\beta_1,...,\beta_{i-1}) = \int_{\tau^2} \prod_{g=1}^{G-1} P\left(\beta_g \middle| \tau_g^2\right) P\left(\tau_g^2\right) d\tau^2$$

where $\beta^T = \left(\beta_1^T,...\beta_{G-1}^T\right)$ and $\tau^T = \left(\tau_1^T,...,\tau_{G-1}^T\right)$.

and $p\left(\beta_g \middle| \tau_g^2\right)$ is $N\left(0, \text{diag}\left\{\tau_g^2\right\}\right)$ and $P\left(\tau_g^2\right)$ is some hyperprior distribution for τ_g^2.

As used herein, when the likelihood function for the probability distribution is based on a categorical ordered logistic regression, the notation for the prior distribution is:

$$P(\beta_1,\beta_2,\cdots,\beta_n) = \int_{\tau} \prod_{i=1}^{N} P\left(\beta_i \middle| \tau_i\right) P\left(\tau_i\right) d\tau$$

where $\beta_1,\beta_2,\cdots,\beta_n$ are component weights, $P\left(\beta_i \middle| \tau_i\right)$ is $N\left(0,\tau_i^2\right)$ and $P\left(\tau_i\right)$ some hyperprior distribution for τ_i.

As used herein, when the likelihood function for the distribution is based on a generalised linear model, the notation for the prior distribution is:

$$p(\beta) = \int_{\tau^2} p\left(\beta \middle| \nu^2\right) p\left(\nu^2\right) d\nu^2$$

wherein ν is a p x 1 vector of hyperparameters, and where $p\left(\beta \middle| \nu^2\right)$ is $N\left(0, \text{diag}\left\{\nu^2\right\}\right)$ and $p\left(\nu^2\right)$ is some prior distribution for ν^2.

As used herein, when the likelihood function for the distribution is based on a hazard model, the notation for the prior distribution is:

$$p\left(\beta^*\right) = \int_{\tau^2} p\left(\beta^* \middle| \nu^2\right) p\left(\nu^2\right) d\nu^2$$

where $p\left(\beta^* \middle| \nu^2\right)$ is $N\left(0, \text{diag}\left\{\nu^2\right\}\right)$ and $p\left(\nu^2\right)$ some hyperprior

distribution for ν^2.

The prior distribution comprises a hyperprior that ensures that zero weights are preferred whenever possible.

Preferably, the hyperprior is a Jeffrey's hyperprior (Kotz and Johnson, 1983).

As discussed above, the prior distribution and the likelihood function are combined to generate a posterior distribution. The posterior distribution is preferably of the form:

$$p(\beta \varphi \nu | y) \alpha L(y|\beta \varphi) p(\beta|\nu^2) p(\nu^2)$$

wherein $L(\underset{\sim}{y}|\underset{\sim}{\beta},\underset{\sim}{\varphi})$ is the likelihood function.

The component weights in the posterior distribution are preferably estimated in an iterative procedure such that the probability density of the posterior distribution is maximised. During the iterative procedure, component weights having a value less than a pre-determined threshold are eliminated, preferably by setting those component weights to zero. This results in elimination of the corresponding component.

Preferably, the iterative procedure is an EM algorithm. The EM algorithm produces a sequence of component weight estimates that converge to give component weights that maximise the probability density of the posterior distribution. The EM algorithm consists of two steps, known as the E or Expectation step and the M, or Maximisation step. In the E step, the expected value of the log-posterior function conditional on the observed data and current parameter values is determined. In the M step, the expected log-posterior function is maximised

to give updated component weight estimates that increase the likelihood. The two steps are alternated until convergence of the E step and the M step is achieved, or in other words, until the expected value and the maximised value of the log-posterior function converge.

It is envisaged that the method of the present invention may be applied to any system from which measurements can be obtained, and preferably systems from which very large amounts of data are generated. Examples of systems to which the method of the present invention may be applied include biological systems, chemical systems, agricultural systems, weather systems, financial systems including, for example, credit risk assessment systems, insurance systems, marketing systems or company record systems, electronic systems, physical systems, astrophysics systems and mechanical systems. For example, in a financial system, the samples may be particular stock and the components may be measurements made on any number of factors which may affect stock prices such as company profits, employee numbers, number of shareholders etc.

The method of the present invention is particularly suitable for use in analysis of biological systems. The method of the present invention may be used to identify subsets of components for classifying samples from any biological system which produces measurable values for the components and in which the components can be uniquely labelled. In other words, the components are labelled or organised in a manner which allows data from one component to be distinguished from data from another component. For example, the components may be spatially organised in, for example, an array which allows data from each component to be distinguished from another by spatial position, or each component may have some unique identification associated with it such as an identification signal or tag. For example, the

components may be bound to individual carriers, each carrier having a detectable identification signature such as quantum dots (see for example, Rosenthal, 2001, Nature Biotech 19: 621-622; Han et al. (2001) Nature Biotechnology 19: 631-635), fluorescent markers (see for example, Fu et al, (1999) Nature Biotechnology 17: 1109-1111), bar-coded tags (see for example, Lockhart and Trulson (2001) Nature Biotechnology 19: 1122-1123).

In a particularly preferred embodiment, the biological system is a biotechnology array. Examples of biotechnology arrays (examples of which are described in Schena et al., 1995, Science 270: 467-470; Lockhart et al. 1996, Nature Biotechnology 14: 1649; US Pat No. 5,569,5880) include oligonucleotide arrays, DNA arrays, DNA microarrays, RNA arrays, RNA microarrays, DNA microchips, RNA microchips, protein arrays, protein microchips, antibody arrays, chemical arrays, carbohydrate arrays, proteomics arrays, lipid arrays. In another embodiment, the biological system may be selected from the group including, for example, DNA or RNA electrophoresis gels, protein or proteomics electrophoresis gels, biomolecular interaction analysis such as Biacore analysis, amino acid analysis, ADMETox screening (see for example High-throughput ADMETox estimation: In Vitro and In Silico approaches (2002), Ferenc Darvas and Gyorgy Dorman (Eds), Biotechniques Press), protein electrophoresis gels and proteomics electrophoresis gels.

The components may be any measurable component of the system. In the case of a biological system, the components may be, for example, genes or portions thereof, DNA sequences, RNA sequences, peptides, proteins, carbohydrate molecules, lipids or mixtures thereof, physiological components, anatomical components, epidemiological components or chemical components.

The training samples may be any data obtained from a system in which the feature of the sample is known. For example, training samples may be data generated from a sample applied to a biological system. For example, when the biological system is a DNA microarray, the training sample may be data obtained from the array following hybridisation of the array with RNA extracted from cells having a known feature, or cDNA synthesised from the RNA extracted from cells, or if the biological system is a proteomics electrophoresis gel, the training sample may be generated from a protein or cell extract applied to the system.

The inventors envisage that the method of the present invention may be used in one embodiment in re-evaluating or evaluating test data from subjects who have presented mixed results in response to a test treatment. Thus, in a second aspect, the present invention provides a method for identifying a subset of components of a subject which are capable of classifying the subject into one of a plurality of predefined groups wherein each group is defined by a response to a test treatment comprising the steps of:

(a) exposing a plurality of subjects to the test treatment and grouping the subjects into response groups based on responses to the treatment;
(b) measuring components of the subjects;
(c) identifying a subset of components that is capable of classifying the subjects into response groups using a statistical analysis method.

Preferably, the statistical analysis method is a method according to the first aspect of the invention.

Once a subset of components has been identified, that subset can be used to classify subjects into groups such as those that are likely to respond to the test treatment

and those that are not. In this manner, the method of the present invention permits treatments to be identified which may be effective for a fraction of the population, and permits identification of that fraction of the population that will be responsive to the test treatment.

In a third aspect, the present invention provides an apparatus for identifying a subset of components of a subject, the subset being capable of classifying the subject into one of a plurality of predefined response groups wherein each response group is formed by exposing a plurality of subjects to a test treatment and grouping the subjects into response groups based on the response to the treatment, the apparatus comprising;

(a) means for receiving measured components of the subjects;
(b) means for identifying a subset of components that is capable of classifying the subjects into response groups using a statistical analysis method.

Preferably, the statistical analysis method is the method according to the first or second aspect.

In a fourth aspect, the present invention provides a method for identifying a subset of components of a subject which are capable of classifying the subject as being responsive or non-responsive to treatment with a test compound comprising the steps of:

(a) exposing a plurality of subjects to the compound and grouping the subjects into response groups based on each subjects response to the compound;
(b) measuring components of the subjects;

(c) identifying a subset of components that is capable of classifying the subjects into response groups using a statistical analysis method.

Preferably, the statistical analysis method is the method according to the first aspect.

In a fifth aspect, the present invention provides an apparatus for identifying a subset of components of a subject, the subset being capable of classifying the subject into one of a plurality of predefined response groups wherein each response group is formed by exposing a plurality of subjects to a compound and grouping the subjects into response groups based on the response to the compound, the apparatus comprising;

(c) means for receiving measured components of the subjects;
(d) means for identifying a subset of components that is capable of classifying the subjects into response groups using a statistical analysis method.

Preferably, the statistical analysis method is the method according to the first or second aspect of the invention.

The components that are measured in the second to fifth aspects of the invention may be, for example, genes or small nucleotide polymorphisms (SNPs), proteins, antibodies, carbohydrates, lipids or any other measureable component of the subject.

In a particularly preferred embodiment, the compound is a pharmaceutical compound or a composition comprising a pharmaceutical compound and a pharmaceutically acceptable carrier.

The identification method of the present invention may be implemented by appropriate computer software and hardware.

In accordance with a sixth aspect, the present invention provides an apparatus for identifying a subset of components of a system from data generated from the system from a plurality of samples from the system, the subset being capable of predicting a feature of a test sample, the apparatus comprising;

(a) means for generating a linear combination of components and component weights in which values for each component are introduced from data generated from a plurality of training samples, each training sample having a known feature;

(b) means for defining a model for the probability distribution of a feature wherein the model is conditional on the linear combination and wherein the model is not a combination of a binomial distribution for a two class response with a probit function linking the linear combination and the expectation of the response;

(c) means for constructing a prior distribution for the component weights of the linear combination comprising a hyperprior having a high probability density close to zero;

(d) means for combining the prior distribution and the model to generate a posterior distribution;

(e) means for identifying a subset of components having component weights that maximise the posterior distribution.

The apparatus may comprise an appropriately programmed computing device.

In accordance with a seventh aspect, the present invention provides a computer program arranged, when loaded onto a computing apparatus, to control the computing apparatus to implement a method in accordance with the first aspect of the present invention.

The computer program may implement any of the preferred algorithms and method steps of the first or second aspect of the present invention which are discussed above.

In accordance with a eighth aspect of the present invention, there is provided a computer readable medium providing a computer program in accordance with the fourth aspect of the present invention.

In accordance with a ninth aspect of the present invention, there is provided a method of testing a sample from a system to identify a feature of the sample, the method comprising the steps of testing for a subset of components which is diagnostic of the feature, the subset of components having been determined by a method in accordance with the first or second aspect of the present invention.

Preferably, the system is a biological system.

In accordance with a tenth aspect of the present invention, there is provided an apparatus for testing a sample from a system to determine a feature of the sample, the apparatus including means for testing for components identified in accordance with the method of the first or second aspect of the present invention.

In accordance with an eleventh aspect, the present invention provides a computer program which when run on a

computing device, is arranged to control the computing device, in a method of identifying components from a system which are capable of predicting a feature of a test sample from the system, and wherein a linear combination of components and component weights is generated from data generated from a plurality of training samples, each training sample having a known feature, and a posterior distribution is generated by combining a prior distribution for the component weights comprising a hyperprior having a high probability distribution close to zero, and a model that is conditional on the linear combination wherein the model is not a combination of a binomial distribution for a two class response with a probit function linking the linear combination and the expectation of the response, to estimate component weights which maximise the posterior distribution.

Where aspects of the present invention are implemented by way of a computing device, it will be appreciated that any appropriate computer hardware e.g. a PC or a mainframe or a networked computing infrastructure, may be used.

In a twelfth aspect, the present invention provides a method for identifying a subset of components of a biological system, the subset being capable of predicting a feature of a test sample from the biological system, the method comprising the steps of:

(a) generating a linear combination of components and component weights in which values for each component are determined from data generated from a plurality of training samples, each training sample having a known feature;

(b) defining a model for the probability distribution of a feature wherein the model is conditional on the linear combination;

(c) constructing a prior distribution for the component weights of the linear combination comprising a hyperprior having a high probability density close to zero;

(d) combining the prior distribution and the model to generate a posterior distribution;

identifying a subset of components having component weights that maximise the posterior distribution.

BRIEF DESCRIPTION OF THE FIGURES

Figure 1 illustrates the results of a permutation test on prediction success of an embodiment of the present invention. Class labels were randomly permuted 200 times, and the analysis repeated for each permutation. The histogram shows the distribution of prediction success under permutation. The number of samples that were correctly classified is shown on the x-axis and the frequency is shown on the y-axis.

Figure 2 illustrates the results of a permutation test on prediction success of an embodiment of the present invention. Class labels were randomly permuted 200 times, and the analysis repeated for each permutation, The histogram shows the distribution of prediction success under permutation of the class labels. The x-axis is the percentage of the total of samples and the y-axis (lambda) is the percent of cases correctly classified.

Figure 3 illustrates a plot of the curve for a generalised linear model used in one embodiment of the method of the invention. The fitted curve (solid line) is produced when 5 components selected by the method are used in the model, and the true curve (dotted line) is

shown as a dotted line, and the data (nf, y-axis) from 200 observations (x-axis) based on the 5 components is shown as circles.

Figure 4 illustrates a plot of the fitted probabilities for a single gene identified using an embodiment of the method of the invention. The gene index is shown on the x-axis and the probability of the sample belonging to a particular ordered class is shown on the y-axis. The lines denote classes as follows: dashed line = class 1, solid line = class 2, dotted line = class 3, dotted and dashed line = class 4.

Figure 5 is a schematic representation of a personal computer used to implement a system according to the present invention.

DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENTS

The present invention identifies preferably a minimum number of components which can be used to identify whether a particular training sample has a particular feature. The minimum number of components is "diagnostic" of that feature, or enables discrimination between samples having a different feature. Essentially, from all the data which is generated from the system, the method of the present invention enables identification of a minimum number of components which can be used to test for a particular feature. Once those components have been identified by this method, the components can be used in future to assess new samples. The method of the present invention utilises a statistical method to eliminate components that are not required to correctly predict the feature.

The inventors have found that component weights of a linear combination of components of data generated from

the training samples can be estimated in such a way as to eliminate the components that are not required to correctly predict the feature of the training sample. The result is that a subset of components are identified which can correctly predict the feature of the training sample. The method of the present invention thus permits identification from a large amount of data a relatively small number of components which are capable of correctly predicting a feature.

The method of the present invention also has the advantage that it requires usage of less computer memory than prior art methods which use joint rather than marginal information on components. Accordingly, the method of the present invention can be performed rapidly on computers such as, for example, laptop machines. By using less memory, the method of the present invention also allows the method to be performed more quickly than prior art methods which use joint (rather than marginal) information on components for analysis of, for example, biological data.

A first embodiment relating to a multiclass logistic regression model will now be described.

A. Multi Class Logistic regression model

The method of this embodiment utilises the training samples in order to identify a subset of components which can classify the training samples into pre-defined groups. Subsequently, knowledge of the subset of components can be used for tests, for example clinical tests, to classify samples into groups such as disease classes. For example, a subset of components of a DNA microarray may be used to group clinical samples into clinically relevant classes such as, for example, healthy or diseased.

In this way, the present invention identifies preferably a minimum number of components which can be used to identify whether a particular training sample belongs to a particular group. The minimum number of components is "diagnostic" of that group, or enables discrimination between groups. Essentially, from all the data which is generated from the system, the method of the present invention enables identification of a minimum number of components which can be used to test for a particular group. Once those components have been identified by this method, the components can be used in future to classify new samples into the groups. The method of the present invention preferably utilises a statistical method to eliminate components that are not required to correctly identify the group the sample belongs to.

The samples are grouped into sample groups (or "classes") based on a pre-determined classification. The classification may be any desired classification by which the training samples are to be grouped. For example, the classification may be whether the training samples are from a leukemia cell or a healthy cell, or that the training samples are obtained from the blood of patients having or not having a certain condition, or that the training samples are from a cell from one of several types of cancer as compared to a normal cell.

In one embodiment, the input data is organised into an $n \times p$ data matrix $X = (x_{ij})$ with n training samples and p components. Typically, p will be much greater than n.

In another embodiment, data matrix X may be replaced by an n x n kernel matrix K to obtain smooth functions of X

as predictors instead of linear predictors. An example of the kernel matrix K is $k_{ij}=\exp(-0.5*(x_i-x_j)^t(x_i-x_j)/\sigma^2)$ where the subscript on x refers to a row number in the matrix X. Ideally, subsets of the columns of K are selected which give sparse representations of these smooth functions. Further examples of kernel matrices are given in table 2 below. (is table 3 needed at all ?)

Associated with each sample class (group) may be a class label y_i, where $y_i = k, k \in \{1,...,G\}$, which indicates which of G sample classes a training sample belongs to. We write the nx1 vector with elements y_i as y. Given the vector $\underset{\sim}{y}$ we can define indicator variables

$$e_{ig} = \begin{cases} 1, & y_i = g \\ 0, & \text{otherwise} \end{cases} \qquad \text{(1A)}$$

In one embodiment, the component weights are estimated using a Bayesian statistical model (see Kotz and Johnson, 1983). Preferably, the weights are estimated by maximising the posterior distribution of the weights given the data generated from each training sample. This results in an objective function to be maximised consisting of two parts. The first part a likelihood function and the second a prior distribution for the weights which ensures that zero weights are preferred whenever possible. In a preferred embodiment, the likelihood function is derived from a multiclass logistic model. Preferably, the likelihood function is computed from the probabilities:

$$p_{ig} = \frac{e^{x_i^T \beta_g}}{\left(1 + \sum_{h=1}^{G-1} e^{x_i^T \beta_h}\right)}, g = 1, \ldots, G-1 \qquad (2A)$$

and

$$p_{iG} = \frac{1}{\left(1 + \sum_{h=1}^{G-1} e^{x_i^T \beta_h}\right)} \qquad (3A)$$

Wherein

p_{ig} is the probability that the training sample with input data X_i will be in sample class g;

$x_i^T \beta_g$ is a linear combination generated from input data from training sample i with component weights β_g;

x_i^T is the components for the i^{th} Row of X and β_g is a set of component weights for sample class g;

Typically, as discussed above, the component weights are estimated in a manner which takes into account the a priori assumption that most of the component weights are zero.

In one embodiment, components weights βg in equation (2A) are estimated in a manner whereby most of the values are zero, yet the samples can still be accurately classified.

In one embodiment, the prior specified for the parameters $\beta_1, \ldots, \beta_{G-1}$ is of the form:

$$P(\beta_1,...,\beta_{G-1}) = \int_{\tau^2} \prod_{g=1}^{G-1} P\left(\beta_g \middle| \tau_g^2\right) P\left(\tau_g^2\right) d\tau^2 \qquad (4A)$$

where $\beta^T = \left(\beta_1^T,...\beta_{G-1}^T\right)$ and $\tau^T = \left(\tau_1^T,...,\tau_{G-1}^T\right)$.

and $p\left(\beta_g \middle| \tau_g^2\right)$ is $N\left(0, \text{diag}\left\{\tau_g^2\right\}\right)$ and $p\left(\tau_g^2\right) \alpha \prod_{i=1}^{n} 1/\tau_{ig}^2$ is a Jeffreys hyperprior, Kotz and Johnson(1983).

In one embodiment, the likelihood function is $L\left(\underset{\sim}{y} \middle| \beta_1,...,\beta_{G-1}\right)$ of the form in equation (8A) and the posterior distribution of β and $\underset{\sim}{\tau}$ given y is

$$p(\beta\tau|y) \alpha\, L(y|\beta)\, p(\beta|\tau)\, p(\tau) \qquad (5A)$$

In one embodiment, the first derivative is determined from the following equation:

$$\frac{\partial \log L}{\partial \beta g} = X^T\left(\underset{\sim}{e}_g - p_g\right), \quad g = 1,...,G-1 \qquad (6A)$$

wherein $\underset{\sim}{e}_g^T = \left(e_{ig}, i = 1,n\right)$, $p_g^T = \left(p_{ig}, i = 1,n\right)$ are vectors indicating membership of sample class g and probability of class g respectively.

In one embodiment, the second derivative is determined from the following algorithm:

$$\frac{\partial^2 \log L}{\partial \beta_g \partial \beta_h} = -X^T diag\left\{\delta_{hg} p_g - p_h p_g\right\} X \qquad (7A)$$

Equation 6 and equation 7 may be derived as follows:

(a) Using equations (1A), (2A) and (3A), the likelihood function of the data can be written as:

$$L=\prod_{i=1}^{n}\left(\prod_{g=1}^{G-1}\left\{\frac{e^{x_i^T\beta_g}}{\left(1+\sum_{g=1}^{G-1}e^{x_i^T\beta_g}\right)}\right\}^{e_{ig}}\left\{\frac{1}{1+\sum_{h=1}^{G-1}e^{x_i^T\beta_h}}\right\}^{e_{iG}}\right) \qquad (8A)$$

(b) Taking logs of equation (8A) and using the fact that $\sum_{h=1}^{G}e_{ih}=1$ for all i gives:

$$l\log L=\sum_{i=1}^{n}\left(\sum_{g=1}^{G-1}e_{ig}x_i^T\beta_g-\log\left(1+\sum_{g=1}^{G-1}e^{x_i^T\beta_g}\right)\right) \qquad (9A)$$

(c) Differentiating equation (9A) with respect to βg gives

$$\frac{\partial\log L}{\partial\beta g}=X^T\left(\underset{\sim}{e}_g-p_g\right),\quad g=1,\ldots,G-1 \qquad (10A)$$

whereby $\underset{\sim}{e}_g^T=\left(e_{ig},i=1,n\right)$, $p_g^T=\left(p_{ig},i=1,n\right)$ are vectors indicating membership of sample class g and probability of class g respectively.

(d) The second derivative of equation (9A) has elements

$$\frac{\partial^2\log L}{\partial\beta_g\partial\beta_h}=-X^T diag\left\{\delta_{hg}p_g-p_hp_g\right\}X \qquad (11A)$$

where

$$\delta_{hg} = \begin{cases} 1, & h = g \\ 0, & \text{otherwise} \end{cases}$$

Component weights which maximise the posterior distribution of the likelihood function may be specified using an EM algorithm comprising an E step and an M step.

Typically, the EM algorithm comprises the steps:

(a) performing an E step by calculating the conditional expected value of the posterior distribution of component weights using the function:

$$Q = \log L - \frac{1}{2}\sum_{g=1}^{G-1} \gamma_g^T \, diag\left\{\hat{\gamma}_g\right\}^{-2} \gamma_g \qquad (12A)$$

where $x_i^T \beta_g = x_i^T P_g \hat{\gamma}_g$ in equation (8A)

(b) performing an M step by applying an iterative procedure to maximise Q as a function of γ whereby:

$$\gamma^{t+1} = \gamma^t - \alpha^t \left(\frac{\partial^2 Q}{\partial \gamma^2}\right)^{-1} \left(\frac{\partial Q}{\partial \gamma}\right) \qquad (13A)$$

where α^t is a step length such that $0 \le \alpha^t \le 1$;

$\beta_g = P_g \gamma_g$;

wherein P_g are matrices of zeroes and ones such that $P^T{}_g \beta_g$ selects non-zero elements of β_g; and

$\gamma = (\gamma_g, \; g=1, \ldots\ldots, G-1)$.

Equation (12A) may be derived as follows:

Calculate the conditional expected value of 5A) given the observed data y and a set of parameter estimates $\hat{\beta}$.

$$Q = Q\left(\beta \middle| \underset{\sim}{y}, \hat{\beta}\right) = \mathrm{E}\left\{\log p\left(\underset{\sim}{\beta}, \underset{\sim}{\tau} \middle| y\right) \middle| y, \hat{\beta}\right\}$$

Consider the case when components of β (and $\hat{\beta}$) are set to zero i.e for $g = 1, \ldots, G-1$, $\beta_g = P_g \gamma_g$ and $\hat{\beta}_g = P_g \hat{\gamma}_g$, where the P_g are matrices of zeroes and ones such that $P_g^T \beta_g$ selects the non zero elements of β_g. In the following we write $\gamma = (\gamma_g, g=1,\ldots,G-1)$. Note that the γ_g are actually subsets of the components of β_g. We use them to keep the notation as simple as possible.

Ignoring terms not involving γ and using (4A), (5A), (9A) we get:

$$Q = \log L - \frac{1}{2} \sum_{g=1}^{G-1} \sum_{i=1}^{n} \mathrm{E}\left\{ \frac{\gamma_{ig}^2}{\tau_{ig}^2} \middle| y, \hat{\underset{\sim}{\gamma}} \right\}$$

$$= \log L - \frac{1}{2} \sum_{g=1}^{G-1} \gamma_g^T \, diag\left\{\hat{\gamma}_g\right\}^{-2} \gamma_g \qquad (14A)$$

where $x_i^T \beta_g = x_i^T P_g \hat{\gamma}_g$ in (8A)

Note that the conditional expectation can be evaluated from first principles given (4A).

The iterative procedure may be derived as follows:

To obtain the derivatives required in (13A), first note that from (8A), (9A) and (10A) we get

$$\frac{\partial Q}{\partial \gamma} = \left(\frac{\partial \beta}{\partial \gamma}\right)\frac{\partial \log L}{\partial \beta} - diag\left\{\hat{\gamma}\right\}^{-2}\gamma$$

$$= \begin{bmatrix} X_1^T(e_1 - p_1) \\ \vdots \\ X_{G-1}^T(e_{G-1} - p_{G-1}) \end{bmatrix} - diag\left\{\hat{\gamma}\right\}^{-2}\gamma \qquad (15A)$$

and

$$\frac{\partial^2 Q}{\partial \gamma^2} = \left(\frac{\partial \beta}{\partial \gamma}\right)\frac{\partial^2 \log L}{\partial^2 \beta}\left(\frac{\partial \beta}{\partial \gamma}\right)^T - diag\left\{\hat{\gamma}\right\}^{-2}$$

$$= -\left\{\begin{pmatrix} X_1^T\Delta_{1,1}X_1 & \cdots & X_1^T\Delta_{1,G-1}X_{G-1} \\ \vdots & & \vdots \\ X_{G-1}\Delta_{G-1,1}X_1 & & X_{G-1}\Delta_{G-1,G-1}X_{G-1} \end{pmatrix} + diag\left\{\hat{\gamma}\right\}^{-2}\right\} \qquad (16A)$$

where

$$\Delta_{gh} = diag\left\{\delta_{gh}p_g - p_g p_h\right\},$$

$$\delta_{gh} = \begin{cases} 1, & g = h \\ 0, & \text{otherwise} \end{cases}$$

and

$$X_g^T = P_g^T X^T, g = 1,\ldots G-1\,. \qquad (17A)$$

In a preferred embodiment, the iterative procedure may be simplified by using only the block diagonals of equation (16A) in equation (13A). For $g=1,...G-1$, this gives:

$$\gamma_g^{t+1} = \gamma_g^t + \alpha^t \left\{ X_g^T \Delta_{gg} X_g + diag\left\{\hat{\gamma}_g\right\}^{-2} \right\}^{-1} \left\{ X_g^T \left(e_g - p_g\right) - diag\left\{\hat{\gamma}_g\right\}^{-1} \gamma_g^t \right\} \quad (18A)$$

Rearranging equation (18A) leads to

$$\gamma_g^{t+1} = \gamma_g^t + \alpha^t diag\left\{\hat{\gamma}_g\right\} \left(Y_g^T \Delta_{gg} Y_g + I\right)^{-1} \left\{ Y_g^T \left(e_g - p_g\right) - diag\left\{\hat{\gamma}_g\right\}^{-1} \gamma_g^t \right\} \quad (19A)$$

where

$$Y_g^T = diag\left\{\hat{\gamma}_g\right\} X_g^T$$

Writing $p(g)$ for the number of columns of Y_g, (19A) requires the inversion of a $p(g) \times p(g)$ matrix which may be quite large. This can be reduced to an $n \times n$ matrix for $p(g) > n$ by noting that:

$$\begin{aligned} \left(Y_g^T \Delta_{gg} Y_g + I\right)^{-1} &= I - Y_g^t \left(Y_g Y_g^T + \Delta_{gg}^{-1}\right)^{-1} Y_g \\ &= I - Z_g^T \left(Z_g Z_g^T + I_n\right)^{-1} Z_g \end{aligned} \quad (20A)$$

where $Z_g = \Delta_{gg}^{\frac{1}{2}} Y_g$. Preferably, (19A) is used when $p(g) < n$ and (19A) with (20A) substituted into equation (19A) is used when $p(g) \geq n$.

In a preferred embodiment, the EM algorithm is performed as follows:

1. Set n=0 , $P_g = I$ and choose an initial value for $\hat{\gamma}^0$. This is done by ridge regression of $\log(p_{ig}/p_{iG})$ on x_i where p_{ig} is chosen to be near one for observations in group g and a small quantity >0 otherwise - subject to the constraint of all probabilities summing to one.

2. Do the E step i.e evaluate $Q = Q\left(\gamma \middle| \underset{\sim}{y}, \hat{\gamma}^n\right)$

3. Set t=0. For $g = 1,\ldots,G-1$ calculate:

a) $\delta_g^t = \gamma_g^{t+1} - \gamma_g^t$ using (19A) with (20A) substituted into (19A) when $p(g) \geq n$.

(b) Writing $\delta^t = \left(\delta_g^t, g = 1,\ldots,G-1\right)$ Do a line search to find the value of α^t in $\underset{\sim}{\gamma}^{t+1} = \underset{\sim}{\gamma}^t + \alpha^t \underset{\sim}{\delta}^t$ which maximises (or simply increases) (12A) as a function of α^t.

c) set $\underset{\sim}{\gamma}^{t+1} = \underset{\sim}{\gamma}^t$ and t=t+1

Repeat steps (a) and (b) until convergence.

This produces γ^{*n+1} say which maximises the current Q function as a function of γ.

For $g = 1,\ldots G-1$ determine $S_g = \left\{ j : \left| \gamma_{jg}^{*n+1} \right| \leq \varepsilon \max_k \left| \gamma_{kg}^{*n+1} \right| \right\}$

Where $\varepsilon \ll 1$, say 10^{-5}. Define P_g so that $\beta_{ig} = 0$ for $i \in S_g$ and

$$\hat{\gamma}_g^{n+1} = \left\{ \gamma_{jg}^{*n+1}, j \notin S_g \right\}$$

This step eliminates variables with small coefficients from the model.

4. Set n=n+1 and go to 2 until convergence.

A second embodiment relating to an categorical ordered logistic regression will now be described.

B. Ordered categories model

The method of this embodiment may utilise the training samples in order to identify a subset of components which can be used to determine whether a test sample belongs to a particular class. For example, to identify genes for assessing a tissue biopsy sample using microarray analysis, microarray data from a series of samples from tissue that has been previously ordered into classes of increasing or decreasing disease severity such as normal tissue, benign tissue, localised tumour and metastasised tumour tissue are used as training samples to identify a subset of components which is capable of indicating the severity of disease associated with the training samples. The subset of components can then be subsequently used to determine whether previously unclassified test samples can be classified as normal, benign, localised tumour or metastasised tumour. Thus, the subset of components is diagnostic of whether a test sample belongs to a particular class within an ordered set of classes. It will be apparent that once the subset of components have been identified, only the subset of components need be tested in future diagnostic procedures to determine to what ordered class a sample belongs.

The method of the invention is particularly suited for the analysis of very large amounts of data. Typically, large data sets obtained from test samples is highly variable and often differs significantly from that obtained from the training samples. The method of the

present invention is able to identify subsets of components from a very large amount of data generated from training samples, and the subset of components identified by the method can then be used to classifying test samples even when the data generated from the test sample is highly variable compared to the data generated from training samples belonging to the same class. Thus, the method of the invention is able to identify a subset of components that are more likely to classify a sample correctly even when the data is of poor quality and/or there is high variability between samples of the same ordered class.

The minimum number of components is "predictive" for that particular ordered class. Essentially, from all the data which is generated from the system, the method of the present invention enables identification of a minimum number of components which can be used to classify the training data. Once those components have been identified by this method, the components can be used in future to classify test samples. The method of the present invention preferably utilises a statistical method to eliminate components that are not required to correctly classify the sample into a class that is a member of an ordered class.

In the following there are N samples, and vectors such as y, z and μ have components y_i, z_i and μ_i for $i = 1,\ldots, N$. Vector multiplication and division is defined component-wise and diag{ · } denotes a diagonal matrix whose diagonals are equal to the argument. We also use $||\cdot||$ to denote Euclidean norm.

Preferably, there are N observations y_i where y_i takes integer values 1,...,G. The values denote classes which are ordered in some way such as for example severity of disease. Associated with each observation there is a set of covariates (variables, e.g gene expression values) arranged into a matrix X with N rows and p columns wherein N is the samples and p the components. The notation x_i^T denotes the i^{th} row of X. Individual (sample) i has probabilities of belonging to class k given by $\pi_{ik} = \pi_k(x_i)$.

Define cumulative probabilities

$$\gamma_{ik} = \sum_{g=1}^{k} \pi_{ik} \quad , \qquad k = 1,...,G$$

Note that γ_{ik} is just the probability that observation i belongs to a class with index less than or equal to k.

Let C be a n by p matrix with elements c_{ij} given by

$$c_{ij} = \begin{cases} 1, \text{ if observation i in class j} \\ 0, \text{ otherwise} \end{cases}$$

and let R be an n by P matrix with elements r_{ij} given by

$$r_{ij} = \sum_{g=1}^{j} c_{ig}$$

These are the cumulative sums of the columns of C within rows.

For independent observations (samples) the likelihood of the data can be written as

$$L = \prod_{i=1}^{N} \prod_{k=1}^{G-1} \left(\frac{\gamma_{ik}}{\gamma_{ik+1}} \right)^{r_{ik}} \left(\frac{\gamma_{ik+1} - \gamma_{ik}}{\gamma_{ik+1}} \right)^{r_{ik+1} - r_{ik}} \qquad (1B)$$

and the log likelihood ($\log(L)$) l can be written as

$$l = \sum_{i=1}^{N} \sum_{k=1}^{G-1} r_{ik} \log\left(\frac{\gamma_{ik}}{\gamma_{ik+1}} \right) + (r_{ik+1} - r_{ik}) \log\left(\frac{\gamma_{ik+1} - \gamma_{ik}}{\gamma_{ik+1}} \right) \qquad (2B)$$

The continuation ratio model may be adopted here as follows:

$$\text{logit}\left(\frac{\gamma_{ik+1}-\gamma_{ik}}{\gamma_{ik+1}}\right)=\text{logit}\left(\frac{\pi_{ik}}{\gamma_{ik+1}}\right)=\theta_k+x_i^T\beta^* \qquad (3B)$$

for k = 2,...,G , see McCullagh and Nelder(1989) and McCullagh(1980) and the discussion therein. Note that

$$\text{logit}\left(\frac{\gamma_{ik+1}-\gamma_{ik}}{\gamma_{ik+1}}\right)=-\text{logit}\left(\frac{\gamma_{ik}}{\gamma_{ik+1}}\right). \qquad (4B)$$

The likelihood is equivalent to a logistic regression likelihood with response vector y and covariate matrix X

$$y=vec\{R\}$$
$$X=\left[B_1^T B_2^T \ldots B_N^T\right]^T$$
$$B_i=\left[I_{G-1}\middle|1_{G-1}x_i^T\right]$$

where I_{G-1} is the G-1 by G-1 identity matrix and 1_{G-1} is a G-1 by 1 vector of ones.
Here vec{ } takes the matrix and forms a vector row by row.

Typically, as discussed above, the component weights are estimated in a manner which takes into account the a priori assumption that most of the component weights are zero.

Following Figueiredo(2001), in order to eliminate redundant variables (covariates), a prior is specified for the parameters β^* by introducing a p x 1 vector of hyperparameters .

Preferably, the prior specified for the component weights is of the form

$$p(\beta^*) = \int_{\nu^2} p(\beta^* | \nu^2) p(\nu^2) d\nu^2$$

(5B)

where $p(\beta^* | \nu^2)$ is $N(0, \text{diag}\{\nu^2\})$ and $p(\nu^2) \alpha \prod_{i=1}^{n} 1/\nu_i^2$ is a Jeffreys prior, Kotz and Johnson(1983). The elements of $\theta = (\theta_2, \ldots \theta_G)^T$ have a non informative prior.

Writing $L(\underset{\sim}{y} | \beta^* \theta)$ for the likelihood function, in a Bayesian framework the posterior distribution of β^*, θ and ν given y is

$$p(\beta^* \theta \nu | y) \alpha L(y | \beta^* \theta) p(\beta^* | \nu) p(\nu) \qquad (6B)$$

Preferably, by treating ν as a vector of missing data, an iterative algorithm such as an EM algorithm (Dempster et al, 1977) can be used to maximise (6B) to produce locally maximum a posteriori estimates of β^* and θ. The prior above is such that the maximum a posteriori estimates will tend to be sparse i.e. if a large number of parameters are redundant, many components of β^* will be zero.
Preferably $\beta^T = (\theta^T, \beta^{*T})$ in the following and diag() denotes a diagonal matrix:

For the ordered categories model above it can be shown that

$$\frac{\partial l}{\partial \beta} = X'(y - \mu) \qquad (7B)$$

$$E\{\frac{\partial^2 l}{\partial \beta^2}\} = -X^{*t}\,\mathrm{diag}\{\mu(1-\mu)\}X^{*} \qquad (8B)$$

where $\mu_i = \exp(x_i^T\beta)/(1+\exp(x_i^T\beta))$ and $\beta^T = (\theta_2,\ldots,\theta_G,\beta^{*T})$.

As mentioned above, the component weights which maximise the posterior distribution may be determined using an iterative procedure. Preferable, the iterative procedure for maximising the posterior distribution of the components and component weights is an EM algorithm, such as, for example, that described in Dempster et al, 1977. Preferably, the EM algorithm is performed as follows:

1. Set n=0, $S_0 = \{1,2,\ldots, p\}$, $\phi^{(0)}$, and $\varepsilon = 10^{-5}$ (say). Set the regularisation parameter κ at a value much greater than 1, say 100. This corresponds to adding $1/\kappa^2$ to the first G-1 diagonal elements of the second derivative matrix in the M step below.

If $p \leq N$ compute initial values β^* by

$$\beta^* = (X^tX+\lambda I)^{-1}X^T g(y+\zeta) \qquad (9B)$$

and if $p > N$ compute initial values β^* by

$$\beta^* = \frac{1}{\lambda}(I - X^T(XX^T+\lambda I)^{-1}X)X^T g(y+\zeta) \qquad (10B)$$

where the ridge parameter λ satisfies $0 < \lambda \leq 1$ and ζ is small and chosen so that the logit link function g is well defined at $y+\zeta$.

2. Define

$$\beta_i^{(n)} = \begin{cases} \beta_i^*, & i \in S_n \\ 0, & \text{otherwise} \end{cases}$$

and let P_n be a matrix of zeroes and ones such that the nonzero elements $\gamma^{(n)}$ of $\beta^{(n)}$ satisfy

$$\gamma^{(n)} = P_n^T \beta^{(n)} \quad , \quad \beta^{(n)} = P_n \gamma^{(n)}$$
$$\gamma = P_n^T \beta \quad , \quad \beta = P_n \gamma$$

Define $w_\beta = (w_{\beta i}, i = 1, p)$, such that

$$w_{\beta i} = \begin{cases} 1, & i \geq G \\ 0, & \text{otherwise} \end{cases}$$

and let $w_\gamma = P_n w_\beta$

3. Perform the E step by calculating

$$Q(\beta \mid \beta^{(n)}) = E\{ \log(p(\beta, v \mid y)) \mid y, \beta^{(n)} \} \\ = l(y \mid \beta) - 0.5 \, (\| (\beta * w_\beta) / \beta^{(n)} \|^2) \qquad (11B)$$

where l is the log likelihood function of y.

Using $\beta = P_n \gamma$ and $\beta^{(n)} = P_n \gamma^{(n)}$ (11B) can be written as

$$Q(\gamma \mid \gamma^{(n)}) = l(y \mid P_n \gamma) - 0.5 \, (\| (\gamma * w_\gamma) / \gamma^{(n)} \|^2) \qquad (12B)$$

4. Do the M step. This can be done with Newton Raphson iterations as follows. Set $\gamma_0 = \gamma^{(n)}$ and for r=0,1,2,... $\gamma_{r+1} = \gamma_r + \alpha_r \delta_r$ where α_r is chosen by a line search algorithm to ensure $Q(\gamma_{r+1} \mid \gamma^{(n)}) > Q(\gamma_r \mid \gamma^{(n)})$.

For $p \leq N$ use

$$\delta_r = \text{diag}(\hat{\gamma}^{(n)}) [Y_n^T V_r^{-1} Y_n + I]^{-1} (Y_n^T z_r - \frac{w_\gamma \gamma_r}{\gamma^{(n)}}) \qquad (13B)$$

where

$$\hat{\gamma}_i^{(n)} = \begin{cases} \gamma_i^{(n)}, & i \geq G \\ \kappa, & \text{otherwise} \end{cases}$$

$$Y_n^T = \mathrm{diag}(\hat{\gamma}^{(n)}) P_n^T X^T$$

$$V_r^{-1} = \mathrm{diag}\{\mu_r(1-\mu_r)\}$$

$$z_r = (y-\mu_r)$$

and $\mu_r = \exp(XP_n\gamma_r)/(1+\exp(XP_n\gamma_r))$.

For p > N use

$$\delta_r = \mathrm{diag}(\hat{\gamma}^{(n)})[I - Y_n^T(Y_n Y_n^T + V_r)^{-1} Y_n](Y_n^T z_r - \frac{w_\gamma \gamma_r}{\gamma^{(n)}}) \qquad (14B)$$

with V_r and z_r defined as before.

Let γ^* be the value of γ_r when some convergence criterion is satisfied e.g

$|| \gamma_r - \gamma_{r+1} || < \varepsilon$ (for example 10^{-5}).

5. Define $\beta^* = P_n\gamma^*$, $S_{n+1} = \{i \geq G: |\beta_i| > \max_{j \geq G}(|\beta_j| * \varepsilon_1)\} \cup \{1,2,...,G-1\}$

where ε_1 is a small constant, say 1e-5. Set n=n+1 .

6. Check convergence. If $|| \gamma^* - \gamma^{(n)} || < \varepsilon_2$ where ε_2 is suitably small then stop, else go to step 2 above.

Recovering the probabilities

Once we have obtained estimates of the parameters β are obtained, calculate

$$a_{ik} = \frac{\hat{\pi}_{ik}}{\hat{\gamma}_{ik}}$$

for i =1,...,N and k = 2,...,G.

Preferably, to obtain the probabilities we use the recursion

$$\pi_{iG} = a_{iG}$$

$$\pi_{ik-1} = \left(\frac{a_{ik-1}}{a_{ik}}\right)(1-a_{ik})\pi_{ik}$$

and the fact that the probabilities sum to one, for i = 1,...,N.

In one embodiment , the covariate matrix X with rows x_i^T can be replaced by a matrix K with ij^{th} element k_{ij} and $k_{ij} = \kappa(x_i - x_j)$ for some kernel function κ . This matrix can also be augmented with a vector of ones. Some example kernels are given in Table 1 below, see Evgeniou et al(1999).

Kernel function	Formula for $\kappa(x - y)$
Gaussian radial basis function	$\exp(- \|\| x - y \|\|^2 / a)$, a>0
Inverse multiquadric	$(\|\| x - y \|\|^2 + c^2)^{-1/2}$
~~m~~Multiquadric	$(\|\| x - y \|\|^2 + c^2)^{1/2}$
Thin plate splines	$\|\| x - y \|\|^{2n+1}$ $\|\| x - y \|\|^{2n} \ln(\|\| x - y \|\|)$
Multi layer perceptron	$\tanh(x \cdot y - \theta)$, for suitable θ
Ploynomial of degree d	$(1 + x \cdot y)^d$
B splines	$B_{2n+1}(x - y)$
Trigonometric polynomials	$\sin((d +1/2)(x-y))/\sin((x-y)/2)$

Table 1: Examples of kernel functions

In Table 1 the last two kernels are preferably one dimensional i.e. for the case when X has only one column. Multivariate versions can be derived from products of these kernel functions. The definition of B_{2n+1} can be found in De Boor(1978). Use of a kernel function

results in estimated probabilities which are smooth (as opposed to transforms of linear) functions of the covariates X. Such models may give a substantially better fit to the data.

A third embodiment relating to a generalised linear model will now be described.

C. Generalised Linear Models

The method of this embodiment utilises the training samples in order to identify a subset of components which can predict the characteristic of a sample. Subsequently, knowledge of the subset of components can be used for tests, for example clinical tests to predict unknown values of the characteristic of interest. For example, a subset of components of a DNA microarray may be used to predict a clinically relevant characteristic such as, for example, a blood glucose level, a white blood cell count, the size of a tumour, tumour growth rate or survival time.

In this way, the present invention identifies preferably a minimum number of components which can be used to predict a characteristic for a particular sample. The minimum number of components is "predictive" for that characteristic. Essentially, from all the data which is generated from the system, the method of the present invention enables identification of a minimum number of components which can be used to predict a particular characteristic. Once those components have been identified by this method, the components can be used in future to predict the characteristic for new samples. The method of the present invention preferably utilises a

statistical method to eliminate components that are not required to correctly predict the characteristic for the sample.

The inventors have found that component weights of a linear combination of components of data generated from the training samples can be estimated in such a way as to eliminate the components that are not required to predict a characteristic for a training sample. The result is that a subset of components are identified which can correctly predict the characteristic for samples in the training set. The method of the present invention thus permits identification from a large amount of data a relatively small number of components which are capable of correctly predicting a characteristic for a training sample, for example, a quantity of interest.

The characteristic may be any characteristic of interest. In one embodiment, the characteristic is a quantity or measure. In another embodiment, they may be the index number of a group, where the samples are grouped into two sample groups (or "classes") based on a pre-determined classification. The classification may be any desired classification by which the training samples are to be grouped. For example, the classification may be whether the training samples are from a leukemia cell or a healthy cell, or that the training samples are obtained from the blood of patients having or not having a certain condition, or that the training samples are from a cell from one of several types of cancer as compared to a normal cell. In another embodiment the characteristic may be a censored survival time, indicating that particular patients have survived for at least a given number of days. In other embodiments the quantity may be any

continuously variable characteristic of the sample which is capable of measurement, for example blood pressure.

In one embodiment, the data may be a quantity y_i, where $i \in \{1,...,N\}$. We write the Nx1 vector with elements y_i as y. We define a p x 1 parameter vector β of component weights (many of which are expected to be zero), and a q x 1 vector of parameters φ (not expected to be zero). Note that q could be zero (i.e. the set of parameters not expected to be zero may be empty).

In one embodiment, the input data is organised into an N x p data matrix $X = (x_{ij})$ with N test training samples and p components. Typically, p will be much greater than N.

In another embodiment, data matrix X may be replaced by an N x N kernel matrix K to obtain smooth functions of X as predictors instead of linear predictors. An example of the kernel matrix K is $k_{ij}=\exp(-0.5*(x_i-x_j)^t(x_i-x_j)/\sigma^2)$ where the subscript on x refers to a row number in the matrix X. Ideally, subsets of the columns of K are selected which give sparse representations of these smooth functions.

Typically, as discussed above, the component weights are estimated in a manner which takes into account the a priori assumption that most of the component weights are zero.

In one embodiment, the prior specified for the component weights is of the form:

$$p(\beta) = \int_{\nu^2} p(\beta \mid \nu^2) p(\nu^2) d\nu^2 \qquad (1C)$$

where $p(\beta \mid \nu^2)$ is $N(0, \mathrm{diag}\{\nu^2\})$ and $p(\nu^2) \alpha \prod_{i=1}^{n} 1/\nu_i^2$ is a Jeffreys prior, Kotz and Johnson(1983). Preferably, an uninformative prior for φ is specified.

The likelihood function defines a model which fits the data based on the distribution of the data. Preferably, the likelihood function is derived from a generalised linear model. For example, the likelihood function $L(\underset{\sim}{y} \mid \beta \varphi)$ may be the form appropriate for a generalised linear model (GLM), such as for example, that described by Nelder and Wedderburn (1972). Preferably, the likelihood function is of the form:

$$l = \log p(y \mid \beta, \varphi) = \sum_{i=1}^{N} \{ \frac{y_i \theta_i - b(\theta_i)}{a_i(\varphi)} + c(y_i, \varphi) \} \qquad (2C)$$

where $y = (y_1, \ldots, y_n)^T$ and $a_i(\phi) = \phi / w_i$ with the w_i being a fixed set of known weights and ϕ a single scale parameter.

Preferably, the likelihood function is specified as follows:
We have

$$E\{y_i\} = b'(\theta_i)$$
$$\mathrm{Var}\{y\} = b''(\theta_i) a_i(\varphi) = \tau_i^2 a_i(\varphi) \qquad (3C)$$

Each observation has a set of covariates x_i and a linear predictor $\eta_i = x_i^T \beta$. The relationship between the mean of the i^{th} observation and its linear predictor is given by

the link function $\eta_i = g(\mu_i) = g(\ b'(\theta_i)\ )$. The inverse of the link is denoted by h, i.e
$\mu_i = b'(\theta_i) = h(\eta_i)$.

In addition to the scale parameter, a generalised linear model may be specified by four components:

- the likelihood or (scaled) deviance function,
- the link function
- the derivative of the link function
- the variance function.

Some common examples of generalised linear models are given in table 2 below.

Table 2

Distribution	Link function $g(\mu)$	Derivative of link function	Variance function	Scale parameter
Gaussian	μ	1	1	yes
Binomial with n trials	$\log\left(\frac{\mu}{1-\mu}\right)$	$\frac{1}{\mu(1-\mu)}$	$\frac{\mu}{n}(1-\mu)$	no
Poisson	$\log\ (\mu)$	$1/\ \mu$	μ	no
Gamma	$1/\ \mu$	$-1/\ \mu^2$	$\mu^{\ 2}$	yes
Inverse Gaussian	$1/\ \mu^2$	$-2/\ \mu^3$	$\mu^{\ 3}$	yes

In another embodiment, the likelihood function is derived from a multiclass logistical model.

In another embodiment, a quasi likelihood model is specified wherein only the link function and variance function are defined. In some instances, such

specification results in the models in the table above. In other instances, no distribution is specified.

In one embodiment, the posterior distribution of β φ and ν given y is estimated using:

$$p(\beta\varphi\nu|y) \alpha L(y|\beta\varphi)p(\beta|\nu)p(\nu)$$

(4C)

wherein $L(\underset{\sim}{y}|\beta\varphi)$ is the likelihood function.

In one embodiment, ν may be treated as a vector of missing data and an iterative procedure used to maximise equation (2C) to produce locally maximum a posteriori estimates of β. The prior of equation (5C) is such that the maximum a posteriori estimates will tend to be sparse i.e. if a large number of parameters are redundant, many components of β will be zero.

As stated above, the component weights which maximise the posterior distribution may be determined using an iterative procedure. Preferable, the iterative procedure for maximising the posterior distribution of the components and component weights is an EM algorithm, such as, for example, that described in Dempster et al, 1977.

In one embodiment, the EM algorithm comprises the steps:

(c) Initialising the algorithm by setting n=0, S0 = {1,2,..., p } , initialise $\varphi^{(0)}$, β^* and applying a value for ε, such as for example $\varepsilon = 10^{-5}$;

(d) Defining

$$\beta_i^{(n)} = \begin{cases} \beta_i^*, & i \varepsilon S_n \\ 0, & \text{otherwise} \end{cases} \qquad (5C)$$

and let Pn be a matrix of zeroes and ones such that the nonzero elements $\gamma(n)$ of $\beta(n)$ satisfy

$$\gamma^{(n)} = P_n^T \beta^{(n)} \quad , \quad \beta^{(n)} = P_n \gamma^{(n)}$$
$$\gamma = P_n^T \beta \quad , \quad \beta = P_n \gamma$$

(e) performing an estimation (E) step by calculating the conditional expected value of the posterior distribution of component weights using the function:

$$Q(\beta \mid \beta^{(n)}, \varphi^{(n)}) = E\{ \log p(\beta, \varphi, \nu \mid y) \mid y, \beta^{(n)}, \varphi^{(n)}\} = l(y \mid \beta, \varphi^{(n)}) - 0.5\, (\| \beta / \beta^{(n)} \|^2) \quad (6C)$$

where l is the log likelihood function of y. Using $\beta = P_n \gamma$ and $\beta^{(n)} = P_n \gamma^{(n)}$ can be written as

$$Q(\gamma \mid \gamma^{(n)}, \varphi^{(n)}) = l(y \mid P_n \gamma, \varphi^{(n)}) - 0.5\, (\| \gamma / \gamma^{(n)} \|^2) \quad (7C)$$

(f) performing a maximisation (M) step by applying an iterative procedure to maximise Q as a function of γ whereby $\gamma_0 = \gamma^{(n)}$ and for r=0,1,2,...

(g) $\gamma_{r+1} = \gamma_r + \alpha_r \delta r$ and where α_r is chosen by a line search algorithm to ensure $Q(\gamma_{r+1} \mid \gamma^{(n)}, \varphi^{(n)}) > Q(\gamma_r \mid \gamma^{(n)}, \varphi^{(n)})$, and

$$\delta_r = \mathrm{diag}(\gamma^{(n)}) [-\mathrm{diag}(\gamma^{(n)}) \frac{\partial^2 l}{\partial^2 \gamma_r} \mathrm{diag}(\gamma^{(n)}) + I]^{-1} (\frac{\partial l}{\partial \gamma_r} - \frac{\gamma_r}{\gamma^{(n)}}) \quad (8C)$$

where:

$$\frac{\partial l}{\partial \gamma_r} = P_n^T \frac{\partial l}{\partial \beta_r} \quad , \quad \frac{\partial^2 l}{\partial^2 \gamma_r} = P_n^T \frac{\partial^2 l}{\partial^2 \beta_r} P_n \quad (9C)$$

for $\beta_r = P_n \gamma_r$.

Let γ^* be the value of γr when some convergence criterion is satisfied, for example, $|| \gamma r - \gamma r+1 || < \varepsilon$ (for example 10^{-5});

(h) Defining $\beta^* = P_n\gamma^*$, $S_{n+1}=\{i: |\beta_i| > \max_j(|\beta_j|*\varepsilon_1)\}$ where ε_1 is a small constant, for example 1e-5.

(i) Set n=n+1 and choose $\varphi^{(n+1)} = \varphi^{(n)} + \kappa_n(\varphi^* - \varphi^{(n)})$ where φ^* satisfies $\frac{\partial}{\partial\varphi}l(y|P_n\gamma^*,\varphi)=0$ and κ_n is a damping factor such that $0< \kappa_n \leq 1$; and

(j) Check convergence. If $||\gamma^* - \gamma^{(n)}|| < \varepsilon_2$ where ε_2 is suitably small then stop, else go to step (b) above.

In another embodiment, step (d) in the maximisation step may be estimated by replacing $\frac{\partial^2 l}{\partial^2\gamma_r}$ with its expectation $E\{\frac{\partial^2 l}{\partial^2\gamma_r}\}$. This is preferred when the model of the data is a generalised linear model.

For generalised linear models the expected value $E\{\frac{\partial^2 l}{\partial^2\gamma_r}\}$ may be calculated as follows:

$$\frac{\partial l}{\partial\beta} = X^T\{\mathrm{diag}(\frac{1}{\tau_i^2}\frac{\partial\mu_i}{\partial\eta_i})(\frac{y_i-\mu_i}{a_i(\varphi)})\} \qquad (10C)$$

where X is the N by p matrix with i^{th} row x_i^T and

$$E\{\frac{\partial^2 l}{\partial^2\beta^2}\} = -E\{(\frac{\partial l}{\partial\beta})(\frac{\partial l}{\partial\beta})^T\}$$
$$= -X^T\mathrm{diag}(a_i(\varphi)\tau_i^2(\frac{\partial\eta_i}{\partial\mu_i})^2)^{-1}X \qquad (11C)$$

This can be written as

$$\frac{\partial l}{\partial \beta}=X^t V^{-1}\left(\frac{\partial \eta}{\partial \mu}\right)(y-\mu) \qquad (12C)$$

$$E\left\{\frac{\partial^2 l}{\partial \beta^2}\right\}=-X^t V^{-1} X \qquad (13C)$$

where $V=\mathrm{diag}(a_i(\varphi)\tau_i^2(\frac{\partial \eta_i}{\partial \mu_i})^2)$.

Preferably, the EM algorithm comprises the steps:

(a) Initialising the algorithm by setting n=0, S0 = {1,2,..., p } , φ(0) , applying a value for ε, such as for example $\varepsilon = 10^{-5}$, and

If p ≤ N compute initial values β* by

$$\beta^*=(X^t X+\lambda I)^{-1} X^T g(y+\zeta) \qquad (14C)$$

and if p > N compute initial values β* by

$$\beta^*=\frac{1}{\lambda}(I-X^T(XX^T+\lambda I)^{-1}X)X^T g(y+\zeta) \qquad (15C)$$

where the ridge parameter λ satisfies $0 < \lambda \leq 1$ and ζ is small and chosen so that the link function g is well defined at y+ζ .

(b) Defining

$$\beta_i^{(n)}=\begin{cases}\beta_i^*, & i \in S_n \\ 0, & \text{otherwise}\end{cases}$$

and let Pn be a matrix of zeroes and ones such that the nonzero elements γ(n) of β(n) satisfy

$$\gamma^{(n)} = P_n^T \beta^{(n)} \quad , \quad \beta^{(n)} = P_n \gamma^{(n)}$$
$$\gamma = P_n^T \beta \quad , \quad \beta = P_n \gamma$$

(c) performing an estimation (E) step by calculating the conditional expected value of the posterior distribution of component weights using the function:

$$Q(\beta \mid \beta^{(n)}, \varphi^{(n)}) = E\{ \log p(\beta, \varphi, \nu \mid y) \mid y, \beta^{(n)}, \varphi^{(n)} \}$$
$$= l(y \mid \beta, \varphi^{(n)}) - 0.5 \, (\| \beta / \beta^{(n)} \|^2) \qquad (16C)$$

where l is the log likelihood function of y. Using $\beta = P_n \gamma$ and $\beta^{(n)} = P_n \gamma^{(n)}$ (16C) can be written as

$$Q(\gamma \mid \gamma^{(n)}, \varphi^{(n)}) = l(y \mid P_n \gamma, \varphi^{(n)}) - 0.5 \, (\| \gamma / \gamma^{(n)} \|^2) \qquad (17C)$$

(d) performing a maximisation (M) step by applying an iterative procedure, for example a Newton Raphson iteration, to maximise Q as a function of γ whereby $\gamma_0 = \gamma^{(n)}$ and for $r=0,1,2,\ldots$ $\gamma_{r+1} = \gamma_r + \alpha_r \delta_r$ where α_r is chosen by a line search algorithm to ensure $Q(\gamma_{r+1} \mid \gamma^{(n)}, \varphi^{(n)}) > Q(\gamma_r \mid \gamma^{(n)}, \varphi^{(n)})$, and

For $p \leq N$ use

$$\delta_r = \mathrm{diag}(\gamma^{(n)}) [Y_n^T V_r^{-1} Y_n + I]^{-1} (Y_n^T V_r^{-1} z_r - \frac{\gamma_r}{\gamma^{(n)}}) \qquad (18C)$$

where

$$Y_n = \mathrm{diag}(\gamma^{(n)}) P_n^T X$$

$$V = \mathrm{diag}(a_i(\varphi) \tau_i^2 (\frac{\partial \eta_i}{\partial \mu_i})^2)$$

$$z = \frac{\partial \eta}{\partial \mu} (y - \mu)$$

and the subscript r denotes that these quantities are evaluated at $\mu = h(X P_n \gamma_r)$.

For $p_r > N$ use

$$\delta_r = \mathrm{diag}(\gamma^{(n)})[I - Y_n^T(Y_n Y_n^T + V_r)^{-1} Y_n](Y_n^T V_r^{-1} z_r - \frac{\gamma_r}{\gamma^{(n)}}) \qquad (19C)$$

with V_r and z_r defined as before.

Let γ^* be the value of γ_r when some convergence criterion is satisfied e.g

$$|| \gamma_r - \gamma_{r+1} || < \varepsilon \quad \text{(for example } 10^{-5}\text{)}.$$

1) Define $\beta^* = P_n\gamma^*$, $S_{n+1}=\{i: |\beta_i| > \max_j(|\beta_j|^*\varepsilon_1)\}$ where ε_1 is a small constant, say 1e-5. Set n=n+1 and choose $\varphi^{n+1} = \varphi^n + \kappa_n(\varphi^* - \varphi^n)$ where ϕ^* satisfies $\frac{\partial}{\partial\varphi} l(y | P_n\gamma^*, \varphi) = 0$ and κ_n is a damping factor such that $0 < \kappa_n \leq 1$. Note that in some cases the scale parameter is known or this equation can be solved explicitly to get an updating equation for φ.

The above embodiments may be extended to incorporate quasi likelihood methods Wedderburn (1974) and McCullagh and Nelder (1983)). In such an embodiment, the same iterative procedure as detailed above will be appropriate, but with Ł the likelihood replaced by a quasi likelihood as shown above and, for example, Table 8.1 in McCullagh and Nelder (1983). In one embodiment there is a modified updating method for the scale parameter φ. To define these models requires specification of the variance function τ^2 , the link function g and the derivative of the link function $\frac{\partial\eta}{\partial\mu}$. Once these are defined the above algorithm can be applied. In one embodiment for quasi likelihood models,

step 5 of the above algorithm is modified so that the scale parameter is updated by calculating

$$\varphi^{(m+1)}=\frac{1}{N}\sum_{i=1}^{N}\frac{(y_i-\mu_i)^2}{\tau_i^2}$$

where μ and τ are evaluated at $\beta^* = P_n\gamma^*$. Preferably, this updating is performed when the number of parameters s in the model is less than N. A divisor of N-s can be used when s is much less than N.

In another embodiment, for both generalised linear models and Quasi likelihood models the covariate matrix X with rows x_i^T can be replaced by a matrix K with ijth element k_{ij} and $k_{ij} = \kappa(x_i-x_j)$ for some kernel function κ . This matrix can also be augmented with a vector of ones. Some example kernels are given in Table 3 below, see Evgeniou et al(1999).

Kernel function	Formula for $\kappa(x - y)$
Gaussian radial basis function	$\exp(- \|\| x - y \|\|^2 / a)$, $a>0$
Inverse multiquadric	$(\|\| x - y \|\|^2 + c^2)^{-1/2}$
multiquadric	$(\|\| x - y \|\|^2 + c^2)^{1/2}$
Thin plate splines	$\|\| x - y \|\|^{2n+1}$ $\|\| x - y \|\|^{2n} \ln(\|\| x - y \|\|)$
Multi layer perceptron	$\tanh(x\cdot y-\theta)$, for suitable θ
Ploynomial of degree d	$(1 + x\cdot y)^d$
B splines	$B_{2n+1}(x - y)$
Trigonometric polynomials	$\sin((d +1/2)(x-y))/\sin((x-y)/2)$

Table 3: Examples of kernel functions

In Table 3 the last two kernels are one dimensional i.e. for the case when X has only one column. Multivariate

versions can be derived from products of these kernel functions. The definition of B_{2n+1} can be found in De Boor(1978). Use of a kernel function in either a generalised linear model or a quasi likelihood model results in mean values which are smooth (as opposed to transforms of linear) functions of the covariates X. Such models may give a substantially better fit to the data.

A fourth embodiment relating to a proportional hazards model will now be described.

D. Proportional Hazard Models

The method of this embodiment may utilise training samples in order to identify a subset of components which are capable of affecting the probability that a defined event (eg death, recovery) will occur within a certain time period. Training samples are obtained from a system and the time measured from when the training sample is obtained to when the event has occurred. Using a statistical method to associate the time to the event with the data obtained from a plurality of training samples, a subset of components may be identified that are capable of predicting the distribution of the time to the event. Subsequently, knowledge of the subset of components can be used for tests, for example clinical tests to predict for example, statistical features of the time to death or time to relapse of a disease. For example, the data from a subset of components of a system may be obtained from a DNA microarray. This data may be used to predict a clinically relevant event such as, for example, expected or median patient survival times, or to

predict onset of certain symptoms, or relapse of a disease.

In this way, the present invention identifies preferably a minimum number of components which can be used to predict the distribution of the time to an event of a system. The minimum number of components is "predictive" for that time to an event. Essentially, from all the data which is generated from the system, the method of the present invention enables identification of a minimum number of components which can be used to predict time to an event. Once those components have been identified by this method, the components can be used in future to predict statistical features of the time to an event of a system from new samples. The method of the present invention preferably utilises a statistical method to eliminate components that are not required to correctly predict the time to an event of a system.

As used herein, "time to an event" refers to a measure of the time from obtaining the sample to which the method of the invention is applied to the time of an event. An event may be any observable event. When the system is a biological system, the event may be, for example, time till failure of a system, time till death, onset of a particular symptom or symptoms, onset or relapse of a condition or disease, change in phenotype or genotype, change in biochemistry, change in morphology of an organism or tissue, change in behaviour.

The samples are associated with a particular time to an event from previous times to an event. The times to an event may be times determined from data obtained from,

for example, patients in which the time from sampling to death is known, or in other words, "genuine" survival times, and patients in which the only information is that the patients were alive when samples were last obtained, or in other words, "censored" survival times indicating that the particular patient has survived for at least a given number of days.

In one embodiment, the input data is organised into an N x p data matrix $X=(x_{ij})$ with N test training samples and p components. Typically, p will be much greater than N.

For example, consider an Nxp data matrix $X=(x_{ij})$ from, for example, a microarray experiment, with N individuals (or samples) and the same p genes for each individual. Preferably, there is associated with each individual $i\,(i=1,2,\cdots,N)$ a variable y_i ($y_i \geq 0$) denoting the time to an event, for example, survival time. For each individual there may also be defined a variable that indicates whether that individual's survival time is a genuine survival time or a censored survival time. Denote the censor indicators as c_i where

$$c_i = \begin{cases} 1, \text{if } y_i \text{ is uncensored} \\ 0, \text{if } y_i \text{ is censored} \end{cases}$$

The Nx1 vector with survival times y_i may be written as $\underset{\sim}{y}$ and the Nx1 vector with censor indicators c_i as $\underset{\sim}{c}$.

Typically, as discussed above, the component weights are estimated in a manner which takes into account the a priori assumption that most of the component weights are zero.

Preferably, the prior specified for the component weights is of the form

$$P(\beta_1,\beta_2,\cdots,\beta_n)=\int_{\tau}\prod_{i=1}^{N}P(\beta_i|\tau_i)P(\tau_i)d\tau \qquad (1D)$$

where $\beta_1,\beta_2,\cdots,\beta_n$ are component weights, $P(\beta_i|\tau_i)$ is $N(0,\tau_i^2)$ and $P(\tau_i)\alpha 1/\tau_i^2$ is a Jeffreys prior (Kotz and Johnson, 1983).

The likelihood function defines a model which fits the data based on the distribution of the data. Preferably, the likelihood function is of the form:

$$Log\ (Partial)\ Likelihood = \sum_{i=1}^{N} g_i(\underset{\sim}{\beta},\underset{\sim}{\varphi};X,\underset{\sim}{y},\underset{\sim}{c}) \qquad (2D)$$

where $\underset{\sim}{\beta}^T=(\beta_1,\beta_2,\cdots,\beta_p)$ and $\underset{\sim}{\varphi}^T=(\varphi_1,\varphi_2,\cdots,\varphi_q)$ are the model parameters. The model defined by the likelihood function may be any model for predicting the time to an event of a system.

In one embodiment, the model defined by the likelihood is Cox's proportional hazards model. Cox's proportional hazards model was introduced by Cox (1972) and may preferably be used as a regression model for survival data. In Cox's proportional hazards model, $\underset{\sim}{\beta}^T$ is a vector of (explanatory) parameters associated with the components. Preferably, the method of the present invention provides for the parsimonious selection (and estimation) from the parameters $\underset{\sim}{\beta}^T=(\beta_1,\beta_2,\cdots,\beta_p)$ for Cox's proportional hazards model given the data X, $\underset{\sim}{y}$ and $\underset{\sim}{c}$.

Application of Cox's proportional hazards model can be problematic in the circumstance where different data is

obtained from a system for the same survival times, or in other words, for cases where tied survival times occur. Tied survival times may be subjected to a pre-processing step that leads to unique survival times. The pre-processing proposed simplifies the ensuing algorithm as it avoids concerns about tied survival times in the subsequent application of Cox's proportional hazards model.

The pre-processing of the survival times applies by adding an extremely small amount of insignificant random noise. Preferably, the procedure is to take sets of tied times and add to each tied time within a set of tied times a random amount that is drawn from a normal distribution that has zero mean and variance proportional to the smallest non-zero distance between sorted survival times. Such pre-processing achieves an elimination of tied times without imposing a draconian perturbation of the survival times.

The pre-processing generates distinct survival times. Preferably, these times may be ordered in increasing magnitude denoted as $\underset{\sim}{t} = \left(t_{(1)}, t_{(2)}, \cdots t_{(N)}\right),\ t_{(i+1)} > t_{(i)}$.

Denote by Z the Nxp matrix that is the re-arrangement of the rows of X where the ordering of the rows of Z corresponds to the ordering induced by the ordering of $\underset{\sim}{t}$; also denote by Z_j the j^{th} row of the matrix Z. Let d be the result of ordering c with the same permutation required to order $\underset{\sim}{t}$.

After pre-processing for tied survival times is taken into account and reference is made to standard texts on survival data analysis (eg Cox and Oakes, 1984),

the likelihood function for the proportional hazards model may preferably be written as

$$L\left(\underset{\sim}{t} \mid \underset{\sim}{\beta}\right) = \prod_{j=1}^{N} \left(\frac{exp\left(Z_j \underset{\sim}{\beta}\right)}{\sum_{i \in \Re_j} exp\left(Z_i \underset{\sim}{\beta}\right)} \right)^{d_j} \qquad (3D)$$

where $\underset{\sim}{\beta}^T = (\beta_1, \beta_2, \cdots, \beta_n)$, Z_j = the j^{th} row of Z, and $\Re_j = \{i : i = j, j+1, \cdots, N\}$ = the risk set at the j^{th} ordered event time $t_{(j)}$.

The logarithm of the likelihood (ie $l = log(L)$) may preferably be written as

$$l\left(\underset{\sim}{t} \mid \underset{\sim}{\beta}\right) = \sum_{i=1}^{N} d_i \left(Z_i \underset{\sim}{\beta} - log\left(\sum_{j \in \Re_i} exp\left(Z_j \underset{\sim}{\beta}\right) \right) \right)$$

$$= \sum_{i=1}^{N} d_i \left(Z_i \underset{\sim}{\beta} - log\left(\sum_{j=1}^{N} \zeta_{i,j} \, exp\left(Z_j \underset{\sim}{\beta}\right) \right) \right), \qquad (4D)$$

where

$$\zeta_{i,j} = \begin{cases} 0, \text{ if } j < i \\ 1, \text{ if } j \geq i \end{cases}$$

Notice that the model is non-parametric in that the parametric form of the survival distribution is not specified - preferably only the ordinal property of the survival times are used (in the determination of the risk sets). As this is a non-parametric case $\underset{\sim}{\varphi}$ is not required (ie q=0).

In another embodiment of the method of the invention, the model defined by the likelihood function is a parametric survival model. Preferably, in a

parametric survival model, $\underset{\sim}{\beta}^T$ is a vector of (explanatory) parameters associated with the components, and $\underset{\sim}{\varphi}^T$ is a vector of parameters associated with the functional form of the survival density function.

Preferably, the method of the invention provides for the parsimonious selection (and estimation) from the parameters $\underset{\sim}{\beta}^T$ and the estimation of $\underset{\sim}{\varphi}^T=(\varphi_1,\varphi_2,\cdots,\varphi_q)$ for parametric survival models given the data X, $\underset{\sim}{y}$ and $\underset{\sim}{c}$.

In applying a parametric survival model, the survival times do not require pre-processing and are denoted as $\underset{\sim}{y}$. The parametric survival model is applied as follows:

Denote by $f(y;\underset{\sim}{\theta},\underset{\sim}{\beta},X)$ the parametric density function of the survival time, denote its survival function by $\mathbb{S}(y;\underset{\sim}{\varphi},\underset{\sim}{\beta},X)=\int_y^\infty f(u;\underset{\sim}{\varphi},\underset{\sim}{\beta},X)du$ where $\underset{\sim}{\varphi}$ are the parameters relevant to the parametric form of the density function and $\underset{\sim}{\beta},X$ are as defined above. The hazard function is defined as $h(y_i;\underset{\sim}{\varphi},\underset{\sim}{\beta},X)=f(y_i;\underset{\sim}{\varphi},\underset{\sim}{\beta},X)/\mathbb{S}(y_i;\underset{\sim}{\varphi},\underset{\sim}{\beta},X)$.

Preferably, the generic formulation of the log-likelihood function, taking censored data into account, is

$$l=\sum_{i=1}^{N}\left\{c_i\log\left(f(y_i;\underset{\sim}{\varphi},\underset{\sim}{\beta},X)\right)+(1-c_i)\log\left(\mathbb{S}(y_i;\underset{\sim}{\varphi},\underset{\sim}{\beta},X)\right)\right\}$$

Reference to standard texts on analysis of survival time data via parametric regression survival models reveals a collection of survival time distributions that may be used. Survival distributions that may be used include, for example, the Weibull, Exponential or Extreme Value distributions.

If the hazard function may be written as $h(y_i;\underset{\sim}{\varphi},\underset{\sim}{\beta},X)=\lambda(y_i;\underset{\sim}{\varphi})exp(X_i\underset{\sim}{\beta})$ then $\mathbb{S}(y_i;\underset{\sim}{\varphi},\underset{\sim}{\beta},X)=exp\left(-\Lambda(y_i;\underset{\sim}{\varphi})e^{X_i\underset{\sim}{\beta}}\right)$ and $f(y_i;\underset{\sim}{\varphi},\underset{\sim}{\beta},X)=\lambda(y_i;\underset{\sim}{\varphi})exp\left(X_i\underset{\sim}{\beta}-\Lambda(y_i)e^{X_i\underset{\sim}{\beta}}\right)$ where

$\Lambda(y_i;\underset{\sim}{\varphi})=\int_{-\infty}^{y_i}\lambda(u;\underset{\sim}{\varphi})du$ is the integrated hazard function and

$\lambda(y_i;\underset{\sim}{\varphi})=\frac{d\Lambda(y_i;\underset{\sim}{\varphi})}{dy_i}$; X_i is the i^{th} row of X.

The Weibull, Exponential and Extreme Value distributions have density and hazard functions that may be written in the form of those presented in the paragraph immediately above.

The application detailed relies in part on an algorithm of Aitken and Clayton (1980) however it permits the user to specify any parametric underlying hazard function.

Following from Aitkin and Clayton (1980) a preferred likelihood function which models a parametric survival model is:

$$l=\sum_{i=1}^{N}\left\{c_i\,log(\mu_i)-\mu_i+c_i\left(log\left(\frac{\lambda(y_i)}{\Lambda(y_i;\underset{\sim}{\varphi})}\right)\right)\right\} \qquad (5D)$$

where $\mu_i=\Lambda(y_i;\underset{\sim}{\varphi})exp(X_i\underset{\sim}{\beta})$. Aitkin and Clayton (1980) note that a consequence of equation (5D) is that the c_i's may be treated as Poisson variates with means μ_i and that the last term in equation (11D) does not depend on $\underset{\sim}{\beta}$ (although it depends on $\underset{\sim}{\varphi}$).

Preferably, the posterior distribution of $\underset{\sim}{\beta}$, $\underset{\sim}{\varphi}$ and $\underset{\sim}{\tau}$ given $\underset{\sim}{y}$ is

$$P(\underset{\sim}{\beta},\underset{\sim}{\varphi},\underset{\sim}{\tau}|\underset{\sim}{y})\,\alpha\,L(\underset{\sim}{y}|\underset{\sim}{\beta},\underset{\sim}{\varphi})P(\underset{\sim}{\beta}|\underset{\sim}{\tau})P(\underset{\sim}{\tau}) \qquad (6D)$$

wherein $L\left(\underset{\sim}{y}\middle|\underset{\sim}{\beta},\underset{\sim}{\varphi}\right)$ is the likelihood function.

In one embodiment, $\underset{\sim}{\tau}$ may be treated as a vector of missing data and an iterative procedure used to maximise equation (6D) to produce a posteriori estimates of $\underset{\sim}{\beta}$. The prior of equation (1D) is such that the maximum a posteriori estimates will tend to be sparse i.e. if a large number of parameters are redundant, many components of $\underset{\sim}{\beta}$ will be zero.

Because a prior expectation exists that many components of $\underset{\sim}{\beta}^T$ are zero, the estimation may be performed in such a way that most of the estimated β_i's are zero and the remaining non-zero estimates provide an adequate explanation of the survival times.

In the context of microarray data this exercise translates to identifying a parsimonious set of genes that provide an adequate explanation for the event times.

As stated above, the component weights which maximise the posterior distribution may be determined using an iterative procedure. Preferable, the iterative procedure for maximising the posterior distribution of the components and component weights is an EM algorithm, such as, for example, that described in Dempster et al, 1977.

In one embodiment, the EM algorithm comprises the steps:

1. Initialising the algorithm by setting $n=0$, $S_0 = \{1, 2, \ldots, p\}$, initialise $\underset{\sim}{\beta}^{(0)} = \underset{\sim}{\beta}^*$, $\underset{\sim}{\varphi}^{(0)}$,

2. Defining

$$\beta_i^{(n)} = \begin{cases} \beta_i^*, & i \varepsilon S_n \\ 0, & \text{otherwise} \end{cases}$$

and let P_n be a matrix of zeroes and ones such that the nonzero elements $\underset{\sim}{\gamma}^{(n)}$ of $\underset{\sim}{\beta}^{(n)}$ satisfy

$$\begin{aligned} \underset{\sim}{\gamma}^{(n)} &= P_n^T \underset{\sim}{\beta}^{(n)} \quad , \quad \underset{\sim}{\beta}^{(n)} = P_n \underset{\sim}{\gamma}^{(n)} \\ \underset{\sim}{\gamma} &= P_n^T \underset{\sim}{\beta} \quad , \quad \underset{\sim}{\beta} = P_n \underset{\sim}{\gamma} \end{aligned} \tag{7D}$$

3. Performing an estimation step by calculating the expected value of the posterior distribution of component weights. This may be performed using the function:

$$\begin{aligned} Q(\underset{\sim}{\beta} \mid \underset{\sim}{\beta}^{(n)}, \varphi^{(n)}) &= E\left\{ \log\left(P\left(\underset{\sim}{\beta}, \underset{\sim}{\varphi}, \tau \mid \underset{\sim}{y} \right) \right) \mid \underset{\sim}{y}, \underset{\sim}{\beta}^{(n)}, \varphi^{(n)} \right\} \\ &= l(\underset{\sim}{y} \mid \underset{\sim}{\beta}, \varphi^{(n)}) - \frac{1}{2} \sum_{i=1}^{N} \left(\frac{\beta_i}{\beta_i^{(n)}} \right)^2 \end{aligned} \tag{8D}$$

where l is the log likelihood function of $\underset{\sim}{y}$. Using $\beta = P_n \gamma$ and $\beta^{(n)} = P_n \gamma^{(n)}$ we have

$$Q(\underset{\sim}{\gamma} \mid \underset{\sim}{\gamma}^{(n)}, \underset{\sim}{\varphi}^{(n)}) = l(\underset{\sim}{t} \mid P_n \underset{\sim}{\gamma}, \underset{\sim}{\varphi}^{(n)}) - \frac{1}{2} \sum_{i=1}^{N} \left(\frac{\gamma_i}{\gamma_i^{(n)}} \right)^2 \tag{9D}$$

4. Performing the maximisation step. This may be performed using Newton Raphson iterations as follows:

Set $\underset{\sim}{\gamma}_0 = \underset{\sim}{\gamma}^{(r)}$ and for r=0,1,2,...

$\underset{\sim}{\gamma}_{r+1} = \underset{\sim}{\gamma}_r + \alpha_r \underset{\sim}{\delta}_r$ where α_r is chosen by a line search algorithm to ensure $Q\left(\underset{\sim}{\gamma}_{r+1} \mid \underset{\sim}{\gamma}^{(n)}, \underset{\sim}{\varphi}^{(n)} \right) > Q\left(\underset{\sim}{\gamma}_r \mid \underset{\sim}{\gamma}^{(n)}, \underset{\sim}{\varphi}^{(n)} \right)$, and

$$\underset{\sim}{\delta}_r = \mathrm{diag}(\underset{\sim}{\gamma}^{(n)})[-\mathrm{diag}(\underset{\sim}{\gamma}^{(n)})\frac{\partial^2 l}{\partial^2 \underset{\sim}{\gamma}_r}\mathrm{diag}(\underset{\sim}{\gamma}^{(n)}) + I]^{-1}(\frac{\partial l}{\partial \underset{\sim}{\gamma}_r} - \frac{\underset{\sim}{\gamma}_r}{\underset{\sim}{\gamma}^{(n)}})$$

$$\text{where } \frac{\partial l}{\partial \underset{\sim}{\gamma}_r} = P_n^T \frac{\partial l}{\partial \underset{\sim}{\beta}_r}, \quad \frac{\partial^2 l}{\partial^2 \underset{\sim}{\gamma}_r} = P_n^T \frac{\partial^2 l}{\partial^2 \underset{\sim}{\beta}_r} P_n \quad \text{for} \quad \underset{\sim}{\beta}_r = P_n \underset{\sim}{\gamma}_r \qquad (10D)$$

Let $\underset{\sim}{\gamma}^*$ be the value of $\underset{\sim}{\gamma}_r$ when some convergence criterion is satisfied e.g $||\underset{\sim}{\gamma}_r - \underset{\sim}{\gamma}_{r+1}|| < \varepsilon$ (for example $\varepsilon = 10^{-5}$).

5. Define $\underset{\sim}{\beta}^* = P_n \underset{\sim}{\gamma}^*$, $S_n = \left\{ i : |\beta_i| > \varepsilon_1 \max_j |\beta_j| \right\}$ where ε_1 is a small constant, say 10^{-5}. Set $n=n+1$, choose $\underset{\sim}{\varphi}^{(n+1)} = \underset{\sim}{\varphi}^{(n)} + \kappa_n \left(\underset{\sim}{\varphi}^* - \underset{\sim}{\varphi}^{(n)} \right)$ where $\underset{\sim}{\varphi}^*$ satisfies $\frac{\partial l\left(\underset{\sim}{y} | P_n \underset{\sim}{\gamma}^*, \underset{\sim}{\varphi} \right)}{\partial \underset{\sim}{\varphi}} = 0$ and κ_n is a damping factor such that $0 < \kappa_n < 1$.

6. Check convergence. If $||\underset{\sim}{\gamma}^* - \underset{\sim}{\gamma}^{(n)}|| < \varepsilon_2$ where ε_2 is suitably small then stop, else go to step 2 above.

In another embodiment, step (4) in the maximisation step may be estimated by replacing $\frac{\partial^2 l}{\partial^2 \gamma_r}$ with its expectation $E\{\frac{\partial^2 l}{\partial^2 \gamma_r}\}$.

In one embodiment, the EM algorithm is applied to maximise the posterior distribution when the model is Cox's proportional hazard's model.

To aid in the exposition of the application of the EM algorithm when the model is Cox's proportional hazards model, it is preferred to define "dynamic weights" and matrices based on these weights. The weights are -

$$w_{i,l} = \frac{\zeta_{i,l} \exp\left(Z_l \underset{\sim}{\beta}\right)}{\sum_{j=1}^{N} \zeta_{i,j} \exp\left(Z_j \underset{\sim}{\beta}\right)},$$

$$w_l^* = \sum_{i=1}^{N} d_i w_{i,l},$$

$$\tilde{w}_l = d_l - w_l^*.$$

Matrices based on these weights are -

$$W_i = \begin{pmatrix} w_{i,1} \\ w_{i,2} \\ \vdots \\ \vdots \\ w_{i,N} \end{pmatrix},$$

$$\tilde{W} = \begin{pmatrix} \tilde{w}_1 \\ \tilde{w}_2 \\ \vdots \\ \vdots \\ \tilde{w}_N \end{pmatrix},$$

$$\Delta\left(W^*\right) = \begin{pmatrix} w_1^* & \cdots & 0 \\ \vdots & \ddots & \vdots \\ 0 & \cdots & w_N^* \end{pmatrix},$$

$$W^{**} = \sum_{i=1}^{N} d_i W_i W_i^T$$

In terms of the matrices of weights the first and second derivatives of l may be written as -

$$\left.\begin{aligned} \frac{\partial l}{\partial \underset{\sim}{\beta}} &= Z^T \tilde{W} \\ \frac{\partial^2 l}{\partial \underset{\sim}{\beta}^2} &= Z^T \left(W^{**} - \Delta\left(W^*\right)\right) Z = Z^T K Z \end{aligned}\right\} \qquad (11D)$$

where $K=W^{**}-\Delta\left(W^{*}\right)$. Note therefore from the transformation matrix P_n described as part of Step (2) of the EM algorithm (Equation 7D) (see also Equations (10D)) it follows that

$$\left.\begin{aligned}\frac{\partial l}{\partial \underset{\sim}{\gamma}_r}&=P_n^T\frac{\partial l}{\partial \underset{\sim}{\beta}_r}=P_n^T Z^T\tilde{W}\\ \frac{\partial^2 l}{\partial \underset{\sim}{\gamma}_r^2}&=P_n^T\frac{\partial^2 l}{\partial \underset{\sim}{\beta}_r^{\,2}}P_n=P_n^T Z^T\left(W^{**}-\Delta\left(W^{*}\right)\right)ZP_n=P_n^T Z^T KZP_n\end{aligned}\right\} \qquad \textbf{(12D)}$$

Preferably, when the model is Cox's proportional hazards model the E step and M step of the EM algorithm are as follows:

1.1. Set $n=0$, $S_0=\{1,2,\cdots,p\}$. Let v be the vector with components

$$\mathrm{v}_i=\begin{cases}1-\varepsilon, & \text{if } c_i=1\\ \varepsilon, & \text{if } c_i=0\end{cases}$$

for some small ε, say .001. Define f to be log(v/t).

If $p \le N$ compute initial values $\underset{\sim}{\beta}^{*}$ by

$$\underset{\sim}{\beta}^{*}=(Z^TZ+\lambda I)^{-1}Z^T\mathrm{f} \quad .$$

If $p > N$ compute initial values $\underset{\sim}{\beta}^{*}$ by

$$\underset{\sim}{\beta}^{*}=\frac{1}{\lambda}(I-Z^T(ZZ^T+\lambda I)^{-1}Z)Z^T\mathrm{f}$$

where the ridge parameter λ satisfies $0 < \lambda \le 1$.

2. Define

$$\beta_i^{(n)}=\begin{cases}\beta_i^{*}, & i\in S_n\\ 0, & \text{otherwise}\end{cases}$$

Let P_n be a matrix of zeroes and ones such that the nonzero elements $\underset{\sim}{\gamma}^{(n)}$ of $\underset{\sim}{\beta}^{(n)}$ satisfy

$$\underset{\sim}{\gamma}^{(n)} = P_n^T \underset{\sim}{\beta}^{(n)} \quad , \quad \underset{\sim}{\beta}^{(n)} = P_n \underset{\sim}{\gamma}^{(n)}$$
$$\underset{\sim}{\gamma} = P_n^T \underset{\sim}{\beta} \quad , \quad \underset{\sim}{\beta} = P_n \underset{\sim}{\gamma}$$

3. Perform the E step by calculating

$$Q(\underset{\sim}{\beta} \mid \underset{\sim}{\beta}^{(n)}) = E\left\{\log\left(P\left(\underset{\sim}{\beta}, \underset{\sim}{\varphi}, \tau \mid \underset{\sim}{t}\right)\right) \mid \underset{\sim}{t}, \underset{\sim}{\beta}^{(n)}\right\}$$
$$= l(\underset{\sim}{t} \mid \underset{\sim}{\beta}) - \frac{1}{2}\sum_{i=1}^{N}\left(\frac{\beta_i}{\beta_i^{(n)}}\right)^2$$

where l is the log likelihood function of $\underset{\sim}{t}$ given by Equation (8D). Using $\beta = P_n \gamma$ and $\beta^{(n)} = P_n \gamma^{(n)}$ we have

$$Q(\underset{\sim}{\gamma} \mid \underset{\sim}{\gamma}^{(n)}) = l(\underset{\sim}{t} \mid P_n \underset{\sim}{\gamma}) - \frac{1}{2}\sum_{i=1}^{N}\left(\frac{\gamma_i}{\gamma_i^{(n)}}\right)^2$$

4. Do the M step. This can be done with Newton Raphson iterations as follows. Set $\underset{\sim}{\gamma}_0 = \underset{\sim}{\gamma}^{(r)}$ and for r=0,1,2,... $\underset{\sim}{\gamma}_{r+1} = \underset{\sim}{\gamma}_r + \alpha_r \underset{\sim}{\delta}_r$ where α_r is chosen by a line search algorithm to ensure $Q\left(\underset{\sim}{\gamma}_{r+1} \mid \underset{\sim}{\gamma}^{(n)}, \underset{\sim}{\varphi}^{(n)}\right) > Q\left(\underset{\sim}{\gamma}_r \mid \underset{\sim}{\gamma}^{(n)}, \underset{\sim}{\varphi}^{(n)}\right)$.

For $p \leq N$ use

$$\underset{\sim}{\delta}_r = diag\left(\underset{\sim}{\gamma}^{(n)}\right)\left(Y^T K Y + I\right)^{-1}\left(Y^T \tilde{W} - diag\left(1/\underset{\sim}{\gamma}^{(n)}\right)\underset{\sim}{\gamma}\right),$$
$$\text{where } Y = ZP_n \text{diag}\left(\underset{\sim}{\gamma}^{(n)}\right).$$

For p > N use

$$\underset{\sim}{\delta}_r = diag\left(\underset{\sim}{\gamma}^{(n)}\right)\left(I - Y^T\left(YY^T + K^{-1}\right)^{-1} Y\right)\left(Y^T \tilde{W} - diag\left(1/\underset{\sim}{\gamma}^{(n)}\right)\underset{\sim}{\gamma}\right)$$

Let γ^* be the value of γ_r when some convergence criterion is satisfied e.g $||\gamma_r - \gamma_{r+1}|| < \varepsilon$ (for example 10^{-5}).

5. Define $\underset{\sim}{\beta}^* = P_n \underset{\sim}{\gamma}^*$, $S_n = \left\{ i : |\beta_i| > \varepsilon_1 \max_j |\beta_j| \right\}$ where ε_1 is a small constant, say 10^{-5}. This step eliminates variables with very small coefficients.

6. Check convergence. If $||\underset{\sim}{\gamma}^* - \underset{\sim}{\gamma}^{(n)}|| < \varepsilon_2$ where ε_2 is suitably small then stop, else set n=n+1, go to step 2 above and repeat procedure until convergence occurs.

In another embodiment the EM algorithm is applied to maximise the posterior distribution when the model is a parametric survival model.

In applying the EM algorithm to the parametic survival model, a consequence of equation (5D) is that the c_i's may be treated as Poisson variates with means μ_i and that the last term in equation (5D) does not depend on β (although it depends on φ).

Note that $log(\mu_i) = log\left(\Lambda\left(y_i; \underset{\sim}{\varphi}\right)\right) + X_i \underset{\sim}{\beta}$ and so it is possible to couch the problem in terms a log-linear model for the Poisson-like mean. Preferably, an iterative maximization of the log-likelihood function is performed where given initial estimates of $\underset{\sim}{\varphi}$ the estimates of $\underset{\sim}{\beta}$ are obtained. Then given these estimates of $\underset{\sim}{\beta}$, updated estimates of $\underset{\sim}{\varphi}$ are obtained. The procedure is continued until convergence occurs.

Applying the posterior distribution described above, we note that (for fixed $\underset{\sim}{\varphi}$)

$$\frac{\partial log(\mu)}{\partial \underset{\sim}{\beta}} = \frac{1}{\mu}\frac{\partial \mu}{\partial \underset{\sim}{\beta}} \Leftrightarrow \frac{\partial \mu}{\partial \underset{\sim}{\beta}} = \mu \frac{\partial log(\mu)}{\partial \underset{\sim}{\beta}} \text{ and } \frac{\partial log(\mu_i)}{\partial \underset{\sim}{\beta}} = X_i \qquad (13D)$$

Consequently from Equations (11D) and (12D) it follows that

$$\frac{\partial l}{\partial \underset{\sim}{\beta}} = X^T\left(\underset{\sim}{c} - \underset{\sim}{\mu}\right) \text{ and } \frac{\partial^2 l}{\partial \underset{\sim}{\beta}^2} = -X^T \operatorname{diag}\left(\underset{\sim}{\mu}\right) X .$$

The versions of Equation (12D) relevant to the parametric survival models are

$$\left.\begin{aligned} \frac{\partial l}{\partial \underset{\sim}{\gamma}_r} &= P_n^T \frac{\partial l}{\partial \underset{\sim}{\beta}_r} = P_n^T X^T\left(\underset{\sim}{c} - \underset{\sim}{\mu}\right) \\ \frac{\partial^2 l}{\partial \underset{\sim}{\gamma}^2_r} &= P_n^T \frac{\partial^2 l}{\partial \underset{\sim}{\beta}_r^2} P_n = -P_n^T X^T \operatorname{diag}\left(\underset{\sim}{\mu}\right) X P_n \end{aligned}\right\} \qquad (14D)$$

To solve for $\underset{\sim}{\varphi}$ after each M step of the EM algorithm (see step 5 below) preferably put $\underset{\sim}{\varphi}^{(n+1)} = \underset{\sim}{\varphi}^{(n+1)} + \kappa_n\left(\underset{\sim}{\varphi}^* - \underset{\sim}{\varphi}^{(n)}\right)$ where $\underset{\sim}{\varphi}^*$ satisfies $\frac{\partial l}{\partial \underset{\sim}{\varphi}} = 0$ for $0 < \kappa_n \leq 1$ and β is fixed at the value obtained from the previous M step.

It is possible to provide an EM algorithm for parameter selection in the context of parametric survival models and microarray data. Preferably, the EM algorithm is as follows:

1. Set $n=0$, $S_0 = \{1, 2, \cdots, p\}$ $\underset{\sim}{\varphi}^{(initial)} = \underset{\sim}{\varphi}^{(0)}$. Let v be the vector with components

$$v_i = \begin{cases} 1-\varepsilon, & \text{if } c_i = 1 \\ \varepsilon, & \text{if } c_i = 0 \end{cases}$$

for some small ε, say for example .001. Define f to be $\log(v/\Lambda(y, \varphi))$.

If $p \leq N$ compute initial values $\underset{\sim}{\beta}^*$ by $\underset{\sim}{\beta}^* = (X^T X + \lambda I)^{-1} X^T f$

If $p > N$ compute initial values $\underset{\sim}{\beta}^*$ by

$$\underset{\sim}{\beta}^* = \frac{1}{\lambda}(I - X^T(XX^T + \lambda I)^{-1} X) X^T f$$

where the ridge parameter λ satisfies $0 < \lambda \leq 1$.

2. Define

$$\beta_i^{(n)} = \begin{cases} \beta_i^*, & i \in S_n \\ 0, & \text{otherwise} \end{cases}$$

Let P_n be a matrix of zeroes and ones such that the nonzero elements $\underset{\sim}{\gamma}^{(n)}$ of $\underset{\sim}{\beta}^{(n)}$ satisfy

$$\underset{\sim}{\gamma}^{(n)} = P_n^T \underset{\sim}{\beta}^{(n)} \quad , \quad \underset{\sim}{\beta}^{(n)} = P_n \underset{\sim}{\gamma}^{(n)}$$
$$\underset{\sim}{\gamma} = P_n^T \underset{\sim}{\beta} \quad , \quad \underset{\sim}{\beta} = P_n \underset{\sim}{\gamma}$$

3. Perform the E step by calculating

$$Q(\underset{\sim}{\beta} \mid \underset{\sim}{\beta}^{(n)}, \underset{\sim}{\varphi}^{(n)}) = E\left\{\log\left(P\left(\underset{\sim}{\beta}, \underset{\sim}{\varphi}, \tau \mid \underset{\sim}{y}\right)\right) \mid \underset{\sim}{y}, \underset{\sim}{\beta}^{(n)}, \underset{\sim}{\varphi}^{(n)}\right\}$$

$$= l(\underset{\sim}{y} \mid \underset{\sim}{\beta}, \underset{\sim}{\varphi}^{(n)}) - \frac{1}{2}\sum_{i=1}^{N}\left(\frac{\beta_i}{\beta_i^{(n)}}\right)^2$$

where ~~L~~ l is the log likelihood function of $\underset{\sim}{y}$ and $\underset{\sim}{\varphi}^{(n)}$.

Using $\beta = P_n \gamma$ and $\beta^{(n)} = P_n \gamma^{(n)}$ we have

$$Q(\underset{\sim}{\gamma} \mid \underset{\sim}{\gamma}^{(n)}, \underset{\sim}{\varphi}^{(n)}) = l(\underset{\sim}{y} \mid P_n \underset{\sim}{\gamma}, \underset{\sim}{\varphi}^{(n)}) - \frac{1}{2}\sum_{i=1}^{N}\left(\frac{\gamma_i}{\gamma_i^{(n)}}\right)^2$$

4. Do the M step. This can be done with Newton Raphson iterations as follows. Set $\underset{\sim}{\gamma}_0 = \underset{\sim}{\gamma}^{(r)}$ and for r=0,1,2,... $\underset{\sim}{\gamma}_{r+1} = \underset{\sim}{\gamma}_r + \alpha_r \underset{\sim}{\delta}_r$ where α_r is chosen by a line search algorithm to ensure $Q\left(\underset{\sim}{\gamma}_{r+1} \mid \underset{\sim}{\gamma}^{(n)}, \underset{\sim}{\varphi}^{(n)}\right) > Q\left(\underset{\sim}{\gamma}_r \mid \underset{\sim}{\gamma}^{(n)}, \underset{\sim}{\varphi}^{(n)}\right)$.

For $p \leq N$ use

$$\underset{\sim}{\delta}_r = -\text{diag}(\underset{\sim}{\gamma}^{(n)})[Y_n^T \text{diag}\left(\underset{\sim}{\mu}\right) Y_n + I]^{-1}(Y_n^T\left(\underset{\sim}{c} - \underset{\sim}{\mu}\right) - \text{diag}\left(1/\underset{\sim}{\gamma}^{(n)}\right)\underset{\sim}{\gamma})$$

where $Y = XP_n \text{diag}\left(\underset{\sim}{\gamma}^{(n)}\right)$.

For p > N use

$$\underset{\sim}{\delta}_r = -\text{diag}\left(\underset{\sim}{\gamma}^{(n)}\right)\left(I - Y^T\left(YY^T + \text{diag}\left(1/\underset{\sim}{\mu}\right)\right)^{-1} Y\right)\left(Y_n^T\left(\underset{\sim}{c} - \underset{\sim}{\mu}\right) - \text{diag}\left(1/\underset{\sim}{\gamma}^{(n)}\right)\underset{\sim}{\gamma}\right)$$

Let γ^* be the value of γ_r when some convergence criterion is satisfied e.g $||\gamma_r - \gamma_{r+1}|| < \varepsilon$ (for example 10^{-5}).

5. Define $\underset{\sim}{\beta}^* = P_n \underset{\sim}{\gamma}^*$, $S_n = \left\{ i : |\beta_i| > \varepsilon_1 \max_j |\beta_j| \right\}$ where ε_1 is a small constant, say 10^{-5}. Set $n=n+1$, choose $\underset{\sim}{\varphi}^{(n+1)} = \underset{\sim}{\varphi}^{(n)} + \kappa_n \left(\underset{\sim}{\varphi}^* - \underset{\sim}{\varphi}^{(n)} \right)$ where $\underset{\sim}{\varphi}^*$ satisfies $\frac{\partial l\left(\underset{\sim}{y} | P_n \underset{\sim}{\gamma}^*, \underset{\sim}{\varphi} \right)}{\partial \underset{\sim}{\varphi}} = 0$ and κ_n is a damping factor such that $0 < \kappa_n < 1$.

6. Check convergence. If $||\underset{\sim}{\gamma}^* - \underset{\sim}{\gamma}^{(n)}|| < \varepsilon_2$ where ε_2 is suitably small then stop, else go to step 2.

In another embodiment, survival times are described by a Weibull survival density function. For the Weibull case $\underset{\sim}{\varphi}$ is preferably one dimensional and

$$\Lambda\left(y; \underset{\sim}{\varphi}\right) = y^{\alpha},$$
$$\lambda\left(y; \underset{\sim}{\varphi}\right) = \alpha y^{\alpha-1},$$
$$\underset{\sim}{\varphi} = \alpha$$

Preferably, $\frac{\partial l}{\partial \alpha} = \frac{N}{\alpha} + \sum_{i=1}^{N} (c_i - \mu_i) log(y_i) = 0$ is solved after each M step so as to provide an updated value of α. Following the steps applied for Cox's proportional hazards model, one may estimate α and select a parsimonious subset of parameters from $\underset{\sim}{\beta}$ that can provide an adequate explanation for the survival times if the survival times follow a Weibull distribution.

Features and advantages of the present invention will become apparent following a description of examples.

EXAMPLES

EXAMPLE 1: Two group Classification for Prostate Cancer using a Logistic regression model

In order to identify subsets of genes capable of classifying tissue into prostate of non-prostate groups, the microarray data set reported and analysed by Luo et al. (2001) was subjected to analysis using the method of the invention in which a binomial logistic regression was used as the model. This data set involves microarray data on 6500 human genes. The study contains 16 subjects known to have prostate cancer and 9 subjects with benign prostatic hyperplasia. However, for brevity of presentation only, 50 genes were selected for analysis. The gene expression ratios for all 50 genes (rows) and 25 patients (columns) are shown in Table 4.

The results of applying the method are given below. The model had G=2 classes and commenced with all 50 genes as potential variables (components or basis functions) in the model. After 21 iterations (see below) the algorithm found 2 genes ,(numbers 36 and 47 of table 5) which gave perfect classification.

To determine whether the result was an artefact due to the large number of genes (variables) available in the data set, we ran a permutation test whereby the class labels were randomly permuted and the algorithm subsequently applied. This was repeated 200 times. Figure 1 gives a histogram of the number of cases correctly classified. The 100% accuracy for the actual data set is in the extreme tail of the permutation distribution with a p value of .015. This suggests the results are not due to chance.

The iteration details for the unpermuted data are shown below:

****

```
Iteration 1   :  13 cycles, criterion -0.127695594930065

misclassification matrix
   1 2
1 16 0
2  0 9
row =true class

Class 1 Number of basis functions in model : 50
************************************************
Iteration 2   :  7 cycles, criterion -1.58111247310685

misclassification matrix
   1 2
1 16 0
2  0 9
row =true class

Class 1 Number of basis functions in model : 50
************************************************
Iteration 3   :  5 cycles, criterion -2.82347006228686

misclassification matrix
   1 2
1 16 0
2  0 9
row =true class

Class 1 Number of basis functions in model : 45
************************************************
Iteration 4   :  4 cycles, criterion -3.0353135992828

misclassification matrix
   1 2
```

```
1 16 0
2  0 9
row =true class

Class  1 : Variables left in model
2 3 8 9 11 12 17 19 23 25 29 31 36 40 42 45 47 48 49
regression coefficients
-0.00111392924172276 -3.66542218865611e-007 -
1.18280157375022e-010 -1.15853525792239e-008 -
2.23611388510839e-01
0 -1.99942263084115e-008 -0.00035412991046087 -
0.844161298425504 -7.02985067116106e-011 -
7.92510183180024e-011
-0.000286751487965763 -8.12273456244463e-008 -
4.57102500405226 -0.000474781601043787 2.81670912477482e-
011 -1.0
2591823605395e-008 1.20451375402485 -0.0120825667151016 -
0.000171130745325351

**********************************************
Iteration 5  :  4 cycles, criterion -2.82549351870821

misclassification matrix
   1 2
1 16 0
2  0 9
row =true class

Class  1 : Variables left in model
2 17 19 29 36 40 47 48 49
regression coefficients
-1.01527560660479e-006 -6.47965734465826e-008 -
0.36354429595162 -2.96434390382785e-008 -5.84197907608526
-8.399
```

36030488418e-008 1.22712881145334 -0.00041963284443207 -
5.78172364089109e-008

****
Iteration 6 : 4 cycles, criterion -2.49714605824366

misclassification matrix
1 2
1 16 0
2 0 9
row =true class

Class 1 : Variables left in model
19 36 47 48
regression coefficients
-0.0598894592370422 -6.95130027598687 1.31485208225331 -
4.34828258633208e-007

****
Iteration 7 : 4 cycles, criterion -2.20181629904024

misclassification matrix
1 2
1 16 0
2 0 9
row =true class

Class 1 : Variables left in model
19 36 47
regression coefficients
-0.00136540505944133 -7.61400108609408 1.40720739106609

****
Iteration 8 : 3 cycles, criterion -2.02147819230974

```
misclassification matrix
   1 2
1 16 0
2  0 9
row =true class

Class  1 : Variables left in model
19 36 47
regression coefficients
-6.3429997893986e-007 -7.9815460139979 1.47084153596716

************************************************
Iteration 9  :  3 cycles, criterion -1.92333435556147

misclassification matrix
   1 2
1 16 0
2  0 9
row =true class

Class  1 : Variables left in model
36 47
regression coefficients
-8.19142602569327 1.50856426381189

************************************************
Iteration 10  :  3 cycles, criterion -1.86996621406647

misclassification matrix
   1 2
1 16 0
2  0 9
row =true class
```

```
Class  1 : Variables left in model
36 47
regression coefficients
-8.30998234780385 1.52999314044398

**********************************************
Iteration 11  :  3 cycles, criterion -1.84085525990757

misclassification matrix
   1 2
1 16 0
2  0 9
row =true class

Class  1 : Variables left in model
36 47
regression coefficients
-8.37612256703144 1.54195991212442

**********************************************
Iteration 12  :  3 cycles, criterion -1.82494385332917

misclassification matrix
   1 2
1 16 0
2  0 9
row =true class

Class  1 : Variables left in model
36 47
regression coefficients
-8.41273310098038 1.54858564046418
```

```
************************************************
Iteration 13  :  2 cycles, criterion -1.81623665404495

misclassification matrix
   1 2
1 16 0
2  0 9
row =true class

Class  1 : Variables left in model
36 47
regression coefficients
-8.43290814197901 1.55223728701224

************************************************
Iteration 14  :  2 cycles, criterion -1.81146858213434

misclassification matrix
   1 2
1 16 0
2  0 9
row =true class

Class  1 : Variables left in model
36 47
regression coefficients
-8.44399866057439 1.5542447583578

************************************************
Iteration 15  :  2 cycles, criterion -1.80885659137866

misclassification matrix
   1 2
1 16 0
```

```
2  0 9
row =true class

Class  1 : Variables left in model
36 47
regression coefficients
-8.45008701361215 1.55534682956666

************************************************
Iteration 16  :  2 cycles, criterion -1.80742542023794

misclassification matrix
   1 2
1 16 0
2  0 9
row =true class

Class  1 : Variables left in model
36 47
regression coefficients
-8.45342684192637 1.55595139130677

************************************************
Iteration 17  :  2 cycles, criterion -1.80664115725287

misclassification matrix
   1 2
1 16 0
2  0 9
row =true class

Class  1 : Variables left in model
36 47
regression coefficients
```

```
-8.45525819006111 1.55628289706596

************************************************
Iteration 18  :  2 cycles, criterion -1.80621136412041

misclassification matrix
   1 2
1 16 0
2  0 9
row =true class

Class  1 : Variables left in model
36 47
regression coefficients
-8.45626215911343 1.55646463370405

************************************************
Iteration 19  :  2 cycles, criterion -1.80597581993879

misclassification matrix
   1 2
1 16 0
2  0 9
row =true class

Class  1 : Variables left in model
36 47
regression coefficients
-8.45681248047617 1.55656425211947

************************************************
Iteration 20  :  2 cycles, criterion -1.80584672964066

misclassification matrix
```

```
   1 2
1 16 0
2  0 9
row =true class

Class  1 : Variables left in model
36 47
regression coefficients
-8.45711411647011 1.55661885392712

************************************************
Iteration 21  :  2 cycles, criterion -1.80577598079056

misclassification matrix
   1 2
1 16 0
2  0 9
row =true class

Class  1 : Variables left in model
36 47
regression coefficients
-8.45727943971564 1.5566487805773
```

Table 4

	Disease State							
	PC	PC	PC	PC	PC	PC	PC	PC
Gene 1	0.84	0.77	1.08	0.89	0.54	0.78	0.81	1.1
Gene 2	0.93	0.92	0.67	1.05	0.62	0.47	0.57	0.46
Gene 3	0.25	0.24	0.6	0.94	0.9	0.59	1.05	1.37
Gene 4	1.02	0.86	0.76	1.11	1.12	0.86	0.83	1.6
Gene 5	0.49	1.4	0.79	2.45	1.14	1.45	0.43	2.07
Gene 6	1.05	1.36	0.97	0.88	1.09	0.76	1.08	0.49
Gene 7	0.77	1.07	0.95	0.76	0.75	0.19	0.64	0.34
Gene 8	0.89	3.92	1.11	0.8	0.63	1.65	1.01	1.23
Gene 9	1.39	0.85	1.34	1.58	2.15	2.25	1.63	1.24
Gene 10	0.63	0.88	0.56	0.94	0.67	0.42	0.6	0.42
Gene 11	0.6	0.62	0.75	0.64	0.49	0.81	0.72	0.82
Gene 12	0.84	0.15	0.67	0.84	0.79	0.93	0.61	0.77
Gene 13	1.24	1.27	1.18	1.87	1.02	1.04	1.3	0.65
Gene 14	1.23	1.04	0.97	0.87	0.81	0.95	1.17	1.13
Gene 15	1.61	1.11	1.33	0.83	0.99	0.63	0.96	0.72
Gene 16	0.59	0.68	1	1.11	1.39	0.86	0.86	0.63
Gene 17	0.47	0.7	0.63	0.76	0.79	1.28	0.56	0.69
Gene 18	1.4	1.4	0.6	0.88	1.33	1.61	2.05	1.05
Gene 19	0.99	0.84	0.86	0.76	0.43	0.79	0.61	0.96
Gene 20	0.73	0.92	0.73	0.73	0.67	0.61	0.81	0.91
Gene 21	1.06	1.07	0.85	1.06	0.79	1.46	0.76	1.1
Gene 22	1.08	0.67	1.16	2.3	0.85	1.55	1.29	1.15
Gene 23	1.29	0.65	1.09	0.86	0.74	1.09	1	1.01
Gene 24	0.9	1	1.04	1.08	0.92	0.99	0.79	0.93
Gene 25	1.25	1.07	1.22	0.94	1.35	1.19	0.98	1.54
Gene 26	0.9	1.34	1.13	0.95	0.53	1.5	0.94	0.8
Gene 27	0.3	0.51	1.45	0.92	1.33	1.61	0.33	0.42
Gene 28	0.39	0.71	0.68	0.57	0.55	0.57	0.6	0.46
Gene 29	1.48	0.67	0.71	1.14	0.95	1.21	0.65	0.74
Gene 30	0.9	0.34	0.9	1.1	0.97	1.01	0.97	1.06
Gene 31	1.16	5.61	0.67	1.03	0.73	1.65	1.14	0.55
Gene 32	0.88	0.86	1.09	0.96	0.58	1.27	0.94	0.76

	Disease State							
	PC	PC	PC	PC	PC	PC	PC	PC
Gene 33	0.73	0.42	1.53	0.55	0.43	0.69	0.66	1.27
Gene 34	0.84	0.76	0.72	1.61	0.73	1.76	0.82	1.88
Gene 35	2.63	1.55	0.31	0.66	0.49	1.62	0.82	1.94
Gene 36	0.15	0.16	0.1	0.22	1.06	0.12	0.22	0.08
Gene 37	3.01	0.76	1.28	0.76	0.24	2.35	0.52	0.4
Gene 38	1.46	0.98	0.94	0.99	1.03	1.51	1.33	1.88
Gene 39	0.87	0.59	0.84	1.47	0.62	1.97	1.15	1.56
Gene 40	0.77	0.93	0.92	1.23	0.86	0.89	0.59	0.82
Gene 41	1.15	0.43	0.47	1	0.67	0.33	0.48	0.29
Gene 42	1.12	0.91	0.71	0.63	1.06	0.61	0.81	0.78
Gene 43	0.86	0.97	1.24	1.09	0.66	1	1.28	0.47
Gene 44	1.33	1.12	1.10	0.92	1.43	1.12	1.15	0.97
Gene 45	1.41	1.15	1.31	1.32	1.32	1.49	1.43	1.4
Gene 46	1.14	1.18	0.86	0.99	0.88	0.97	0.92	1.32
Gene 47	5.08	4.95	7.08	11.26	7.59	9.59	2.68	2.55
Gene 48	0.66	0.72	1.18	0.92	0.91	1.27	1.16	1.27
Gene 49	1.06	1.15	1.37	1.67	1.05	0.92	1	0.96
Gene 50	32.91	12.32	8.35	4.93	10.99	14.22	4.72	3.15

	Disease State							
	PC	PC	PC	PC	PC	PC	PC	PC
Gene 1	1.24	1.43	0.43	1.26	0.89	1.16	1.31	2.3
Gene 2	0.3	0.82	2.55	0.39	0.87	1.16	0.55	0.63
Gene 3	1.17	0.58	0.5	0.6	0.36	1.85	0.72	1.07
Gene 4	1.56	1.24	1.34	1.84	1.08	1.06	1.47	0.87
Gene 5	0.69	0.92	1.16	1.94	1.34	0.92	1.42	6.99
Gene 6	0.23	0.98	0.57	0.71	0.57	0.73	0.81	0.84
Gene 7	0.4	3.68	0.49	0.23	1.05	0.54	0.79	1.34
Gene 8	1.23	0.61	2.04	1.3	0.79	1.32	3.96	1.64
Gene 9	0.69	1.15	2.6	2.24	1.95	1.47	1.3	1.54
Gene 10	0.48	0.39	0.44	0.8	0.58	0.79	0.42	1.85
Gene 11	0.57	0.58	0.82	0.69	0.67	0.6	0.77	1.09
Gene 12	0.49	0.94	0.85	0.81	1.04	0.83	0.83	0.35

	Disease State							
	PC	PC	PC	PC	PC	PC	PC	PC
Gene 13	1.02	1.16	0.76	1.49	1.38	1.29	1.47	1.19
Gene 14	1.15	0.85	1.38	1.23	2.06	0.72	1.16	0.98
Gene 15	0.2	0.52	1.1	0.39	0.76	0.37	1.18	2.06
Gene 16	0.68	1.32	0.99	0.78	1.16	0.9	1.03	1.67
Gene 17	0.41	0.73	1.25	0.79	0.9	0.55	0.93	0.68
Gene 18	0.25	0.56	1.71	0.86	3.07	0.99	2.42	2.28
Gene 19	0.48	0.48	0.94	0.1	0.45	0.36	0.37	1.06
Gene 20	0.46	0.5	0.46	0.4	0.47	0.78	0.57	1.31
Gene 21	1.19	1.55	1.16	1.27	1.54	0.93	1.61	0.36
Gene 22	2	0.84	0.86	1.7	1.01	0.6	2.22	0.99
Gene 23	1.03	0.63	1.45	0.72	0.94	1.94	1.06	1.21
Gene 24	0.87	1.11	0.86	1.37	1.18	0.8	1.19	1.74
Gene 25	2.24	1.29	1.27	0.9	1.46	1.02	1.04	1.27
Gene 26	0.28	0.75	0.89	0.85	0.66	1.52	0.43	0.58
Gene 27	6.08	0.41	0.43	5.22	3	1.85	0.17	0.91
Gene 28	0.4	1.07	0.93	1.63	0.92	0.46	0.67	0.95
Gene 29	2.66	0.67	0.84	2.46	0.74	1.5	1.86	2.41
Gene 30	1.17	0.55	0.83	0.98	1.12	1.52	1.29	1.01
Gene 31	0.43	0.3	0.56	1.68	0.81	0.83	1.33	1.39
Gene 32	0.59	1.1	1.86	1.08	1.32	0.59	1.17	0.65
Gene 33	1.16	0.63	0.81	1.04	0.56	0.25	0.61	0.26
Gene 34	1.32	0.63	1.18	0.82	0.73	0.23	0.81	0.45
Gene 35	1.36	0.91	1.09	1.06	0.99	1.16	0.55	2.39
Gene 36	0.2	0.23	0.11	0.13	0.18	0.12	0.24	0.59
Gene 37	0.14	3.68	1.45	5.22	2.06	2.48	3.27	0.59
Gene 38	1.64	0.46	2.15	2	1.66	0.87	2.78	1.27
Gene 39	1.55	0.71	1.1	1.63	1.19	1.48	3.31	2.14
Gene 40	0.74	0.39	0.47	1.14	0.87	0.9	1.16	2.42
Gene 41	6.08	3.68	1.04	0.36	2.03	1.85	1.24	3.52
Gene 42	0.4	4.67	1.3	5.22	1	1.07	0.47	3.52
Gene 43	0.76	0.6	1.14	0.54	0.88	0.73	0.93	0.69
Gene 44	1.07	0.84	1.03	0.95	1.36	0.89	1.15	1.20
Gene 45	1.16	1.13	1.25	1.4	1.5	1.55	2.21	0.99
Gene 46	1.08	0.87	0.66	0.79	0.61	1.06	1.46	0.98
Gene 47	4.29	2.51	5.7	6.08	7.01	5.58	6.28	5.58

	Disease State							
	PC	PC	PC	PC	PC	PC	PC	PC
Gene 48	1.18	1.22	1.35	1.31	1.66	1.2	1.13	1.93
Gene 49	1.3	0.76	0.98	0.58	1.08	0.74	0.83	0.65
Gene 50	1.53	1.79	6.49	5.28	4.52	5.41	22.03	4.6

	Disease State								
	BPH	BPH	BPH	BPH	BPH	BPH	BPH	BPH	BPH
Gene 1	3.91	2.56	0.52	1.33	0.93	0.97	1.68	1.29	0.98
Gene 2	4	0.31	7.02	1.61	0.81	0.85	1.06	0.99	0.87
Gene 3	0.91	10.51	0.57	2.56	1.37	1.1	1.2	1.34	0.91
Gene 4	0.85	0.89	1	1.2	1.05	1.09	1.27	1.18	0.68
Gene 5	0.91	4.2	0.45	0.47	1.11	1.48	0.81	2.3	1.13
Gene 6	1.72	1.44	1.13	0.89	1.03	1.25	1.13	1.15	1
Gene 7	0.8	0.74	1.25	1.19	0.94	1.01	1.04	0.92	1.15
Gene 8	1.18	3.69	1.86	0.99	1.12	1.46	1.56	1.53	0.84
Gene 9	1.27	1.28	1.49	1.36	0.87	1.21	0.84	1.02	0.95
Gene 10	0.9	0.99	0.88	0.93	0.64	0.87	0.72	0.76	0.7
Gene 11	0.88	1.12	1.02	0.96	1	0.96	1.1	0.79	0.9
Gene 12	1.03	0.95	1.11	1.29	0.76	1.02	0.93	0.89	1.26
Gene 13	1.02	0.91	1.02	0.87	0.94	1.04	0.93	0.92	1.05
Gene 14	0.71	1.32	1.2	0.92	1.05	1.02	0.98	0.93	0.92
Gene 15	0.75	0.82	0.57	0.76	0.91	0.76	0.86	1.09	1.22
Gene 16	1.02	1.05	1.19	1.01	0.63	0.99	1.03	1.01	0.8
Gene 17	2.14	3.42	1.34	1.61	0.58	0.86	0.67	0.82	0.77
Gene 18	0.54	1.74	2.85	0.7	1.24	1.05	1.35	1.1	0.99
Gene 19	1.41	1.27	0.81	0.81	1.48	1.19	1.23	1.16	0.86
Gene 20	0.72	0.77	0.87	0.66	0.75	0.87	0.89	0.73	0.84
Gene 21	1.11	0.63	0.95	1.16	0.95	1.16	1.62	1.03	0.91
Gene 22	0.89	0.91	1.22	1.19	0.95	1.24	1.27	1.11	0.95
Gene 23	0.86	2.77	0.92	1.2	1.15	1.72	1.71	1.45	1.09
Gene 24	0.8	0.87	0.99	0.78	0.95	0.87	0.9	0.92	0.92
Gene 25	1.51	1.17	1.19	1.38	0.91	1.21	1.43	1.07	0.92
Gene 26	1.42	2.33	0.96	1.43	0.96	1.42	1.59	1.31	0.81
Gene 27	2	0.79	0.7	1.18	0.88	0.78	0.71	0.93	0.99

	Disease State								
	BPH	BPH	BPH	BPH	BPH	BPH	BPH	BPH	BPH
Gene 28	2.1	0.76	1.04	0.67	0.59	0.85	0.9	1.08	0.72
Gene 29	0.74	1.2	1.01	1.08	1.08	1.21	1.36	1.38	1.19
Gene 30	1.02	5.06	1.13	1.03	0.94	1.23	1.04	1.04	1.08
Gene 31	0.64	2.18	1.71	0.87	1.29	2.09	1.85	1.29	1.89
Gene 32	0.94	0.82	1.29	1.61	0.65	0.9	1.45	1.07	1.42
Gene 33	0.71	0.65	0.69	0.65	1.14	1.05	1.1	0.85	0.81
Gene 34	1.16	0.89	0.85	0.81	1.52	1.23	1.32	1.15	0.98
Gene 35	1.14	1.09	0.72	0.55	1.35	1.39	1.59	1.48	0.91
Gene 36	0.65	0.73	0.71	0.45	0.49	0.81	0.67	0.61	0.64
Gene 37	0.79	0.41	0.9	1.66	0.99	1.01	1.03	0.88	0.82
Gene 38	1.11	0.78	1.55	0.79	0.96	1.61	1.51	1.34	1.18
Gene 39	0.87	0.91	0.93	1.15	1.1	1.49	1.27	1.39	1.36
Gene 40	0.96	1.11	0.76	1.83	0.83	0.94	0.93	0.81	0.78
Gene 41	1.78	3.68	1.75	1.44	0.88	1.23	1.31	1.05	1.4
Gene 42	0.99	0.38	1.72	2.29	0.98	1	1.07	1.18	1.02
Gene 43	0.67	0.81	1.38	0.8	0.82	0.97	0.88	0.75	0.88
Gene 44	0.75	0.72	0.62	1.03	0.89	1.12	1.64	1.35	0.64
Gene 45	1.03	0.85	1	0.81	1.27	1.29	1.34	1.4	1.27
Gene 46	0.79	5.83	0.65	0.74	0.48	0.67	1.17	0.83	0.09
Gene 47	1.45	1.04	0.74	0.91	1.37	1.05	1.1	1.85	1.68
Gene 48	1.47	1.66	1.61	1.27	2.96	2.77	2.44	12.77	5.04
Gene 49	0.79	0.79	1.3	0.82	2.96	2.77	2.44	2	10.91
Gene 50	3.45	0.93	0.85	3.2	1.04	1.11	1.12	1.16	1.09

Example 2: Two Group Classification Using a Large Data set and a binomial logistic regression model.

In order to identify subsets of genes capable of classifying tissue into different clinical types of lymphoma, the data set reported and analysed in Alizadeh, A.A., et al. (2000) Distinct types of diffuse large B-cell lymphoma identified by gene expression profiling. Nature 403:503-511 was subjected to analysis using the

method of the invention in which a binomial logistic regression was used as the model.

In the data set, there are n=4026 genes and n=42 samples. In the following DLBCL refers to "Diffuse large B cell Lymphoma". The samples have been classified into two disease types GC B-like DLBCL (21 samples) and Activated B-like DLBCL (21 samples). We use this set to illustrate the use of the above methodology for rapidly discovering genes which are diagnostic of different disease types.

The results of applying the methodology are given below. The model had G=2 classes and commenced with all genes as potential variables (basis functions) in the model. After 20 iterations the algorithm found 2 gene, numbers 1281 and 1312 (GENE3332X and GENE3258X) which gave the misclassification (table 5) below, and an overall classification success rate of 98%. This example ran in about 20 seconds on a laptop machine.

Table 5

	Predicted class 1	Predicted class 2
True class 1	20	1
True class 2	0	21

To determine whether the result was an artefact due to the large number of genes (variables) available in the data set, we ran a permutation test whereby the class labels were randomly permuted and the algorithm subsequently applied. This was repeated 1000 times. Figure 2 gives a histogram of the percent of cases correctly classified (lambda). The 97.6% accuracy for the actual data set is in the extreme tail of the permutation distribution with a p value of .013. These observations suggests the results are not due to chance.

Example 3: Multi group Classification

In order to identify genes capable of classifying samples into one of a multitude of classes, the data set reported and analyzed in Yeoh et al. Cancer Cell v1: 133-143 (2002) was subjected to analysis using the method of the invention in which a likelihood was used based on a multinomial logistic regression. The same pre-processing as described in Yeoh et al has been applied. This consisted of the following:

- drop the following 8 arrays: BCR.ABL.R4, MLL.R5, Normal.R4, T.ALL.R7, T.ALL.R8,Hyperdip.50.2M.3 ,Hypodip.2M.3 , and Hypodip.2M.2
- set the mean response value of each array to 2500
- thresholding - values over 45000 are set to 45000 values less than 100 are set to 1
- genes with less than 0.01 present are eliminated - this amounted to 1607 genes
- genes for which the difference between the maximum and the minimum value was less than 100 are eliminated (1604 genes)

After preprocessing there are n=11005 genes and n= 248 samples. The samples have been classified into 6 disease types:

1. BCR-ABL;
2. E2A-PBX1;
3. Hyperdip> 50;
4. MLL;
5. T-ALL and
6. TEL-AML1.

This set was used to illustrate the use of the method for rapidly discovering genes which are diagnostic of different disease types. The results of applying the methodology are given below. The model had G=6 classes and commenced with all genes as potential

variables (basis functions) in the model. After 20 iterations the algorithm found that the following 10 genes separated the classes:

X35823.at, X32562.at, X430.at, X39039.s.at, X39756.g.at, X1287.at, X40518.at, X38319.at, X41442.at, X1077.at.

A 15-fold cross validation gave the misclassification table below (Table 6), with 94% classification success:

Table 6

subtype	1	2	3	4	5	6
BCR.ABL	10	1	3	1	0	0
E2A.PBX1	0	27	0	0	0	0
Hyperdip>50	3	0	60	1	0	0
MLL	1	1	2	16	1	2
T-ALL	0	0	1	0	42	0
TEL-AML1	0	0	0	1	0	78

Confusion matrix for Multigroup classification cross-validation (15-fold)

A permutation test (permuting the class labels) showed that the cross validated error rate of 0.94% is highly significant ($p = 0.00$).

Example 4: Standard regression using a generalised linear model

This example illustrates how the method can be implemented in a generalised linear model framework. This example is a standard regression problem with 200 observations and 41 variables(basis functions). The true curve is observed with error (or noise) and is known to depend on only some of the variables. The responses are

continuous and normally distributed. We analyse these data using our algorithm for generalised linear model variable selection.

This is a generalised linear model with:
Link function: $g(\mu) = \mu$
Derivative of link function: $\frac{\partial \eta}{\partial \mu} = 1$
Variance function: $\tau^2 = 1$
Scale parameter $\varphi = \sigma^2$
Deviance (likelihood function): $-\frac{N}{2}\log(\sigma^2) - 0.5*\sum_{i=1}^{N}\frac{(y_i-\mu_i)^2}{\sigma^2}$
The updating formula for σ^2 is

$$(\sigma^2)^{n+1} = \frac{1}{N}\sum_{i=1}^{N}(y_i-\mu_i^*)^2$$

where μ_i^* is the mean evaluated at β^* in step 5 of the algorithm.

The output of the algorithm is given below.

EM Iteration: 1 expected post: -55.45434 basis fns 41
sigma squared 0.5607509

EM Iteration: 2 expected post: -43.96193 basis fns 41
sigma squared 0.5773566

EM Iteration: 3 expected post: -48.87198 basis fns 39
sigma squared 0.5943395

EM Iteration: 4 expected post: -52.79632 basis fns 31
sigma squared 0.6072137

EM Iteration: 5 expected post: -55.18578 basis fns 28
sigma squared 0.6161707

EM Iteration: 6 expected post: -56.5303 basis fns 23

```
sigma squared 0.6224545

EM Iteration:  7 expected post:  -57.47589 basis fns 17
sigma squared 0.626674

EM Iteration:  8 expected post:  -58.0566 basis fns 15
sigma squared 0.6293923

EM Iteration:  9 expected post:  -58.41912 basis fns 13
sigma squared 0.6315789

EM Iteration:  10 expected post:  -58.6923 basis fns 11
sigma squared 0.633089

EM Iteration:  11 expected post:  -58.88766 basis fns 10
sigma squared 0.6343793

EM Iteration:  12 expected post:  -59.05261 basis fns 10
sigma squared 0.635997

EM Iteration:  13 expected post:  -59.24126 basis fns 9
sigma squared 0.6381456

EM Iteration:  14 expected post:  -59.47668 basis fns 9
sigma squared 0.640962

EM Iteration:  15 expected post:  -59.7677 basis fns 9
sigma squared 0.6443392

EM Iteration:  16 expected post:  -60.10277 basis fns 9
sigma squared 0.6477088

EM Iteration:  17 expected post:  -60.44193 basis fns 9
sigma squared 0.6508144
```

EM Iteration: 18 expected post: -60.7684 basis fns 9
sigma squared 0.6539145

EM Iteration: 19 expected post: -61.09251 basis fns 9
sigma squared 0.6565873

EM Iteration: 20 expected post: -61.38427 basis fns 8
sigma squared 0.6589498

EM Iteration: 21 expected post: -61.65061 basis fns 8
sigma squared 0.6615976

EM Iteration: 22 expected post: -61.92217 basis fns 8
sigma squared 0.664281

EM Iteration: 23 expected post: -62.17683 basis fns 7
sigma squared 0.6663748

EM Iteration: 24 expected post: -62.37402 basis fns 7
sigma squared 0.6679655

EM Iteration: 25 expected post: -62.51645 basis fns 7
sigma squared 0.6689011

EM Iteration: 26 expected post: -62.59567 basis fns 6
sigma squared 0.6689011

EM Iteration: 27 expected post: -62.6151 basis fns 6
sigma squared 0.6690962

EM Iteration: 28 expected post: -62.61717 basis fns 6
sigma squared 0.6691031

EM Iteration: 29 expected post: -62.61739 basis fns 5 sigma squared 0.6691035

The algorithm converges with a model involving 5 of the 41 basis vectors (variables). A plot of the fitted curve (solid line) for the model with 5 variables (basis functions) selected by the algorithm , the true curve (dotted line) and the noisy data are given in Figure 3 where the y variable is denoted nf.

Example 5: Small linear regression example using a generalized linear model

This example is similar to example 4, but for brevity, a smaller number of variables (10) is used. This allows the full data set to be tabulated (see Table 7).The dependent variable is a function of the first four variables only, the remaining variables are noise.

The data were analysed as a generalised linear model, with identity link, constant variance, and a normal response. After 12 iterations the algorithm converged to a solution involving just the four variables known to have predictive information, and discarding all six of the noise variables.

Table 7

Predictor Variables										Dependent
V1	V2	V3	V4	V5	V6	V7	V8	V9	V10	Variable
0.778801	0.852144	0.913931	0.960789	0.990050	1.000000	0.990050	0.960789	0.913931	0.852144	0.378571
0.778801	0.697676	0.612626	0.527292	0.444858	0.367879	0.298197	0.236928	0.184520	0.140858	2.832704
0.105399	0.077305	0.055576	0.039164	0.027052	0.018316	0.012155	0.007907	0.005042	0.003151	3.359711
0.001930	0.001159	0.000682	0.000394	0.000223	0.000123	0.000067	0.000036	0.000019	0.000010	2.170812
0.000005	0.000002	0.000001	0.000001	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	3.440226
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	2.424206
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	-0.10464
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	3.672

Predictor Variables										Dependent
V1	V2	V3	V4	V5	V6	V7	V8	V9	V10	Variable
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	2.003438
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.970833
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	1.28257
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	1.085955
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	-0.30299
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.050082
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.457228
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.117205
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	-0.22729
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	2.094908
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	1.084125
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.598052
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	-0.22954
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000001	0.000001	0.02262
0.000002	0.000005	0.000010	0.000019	0.000036	0.000067	0.000123	0.000223	0.000394	0.000682	-1.5989
0.001159	0.001930	0.003151	0.005042	0.007907	0.012155	0.018316	0.027052	0.039164	0.055576	0.163323
0.077305	0.105399	0.140858	0.184520	0.236928	0.298197	0.367879	0.444858	0.527292	0.612626	-0.46697
0.697676	0.778801	0.852144	0.913931	0.960789	0.990050	1.000000	0.990050	0.960789	0.913931	1.104836
0.852144	0.778801	0.697676	0.612626	0.527292	0.444858	0.367879	0.298197	0.236928	0.184520	0.257917
0.140858	0.105399	0.077305	0.055576	0.039164	0.027052	0.018316	0.012155	0.007907	0.005042	0.762435
0.003151	0.001930	0.001159	0.000682	0.000394	0.000223	0.000123	0.000067	0.000036	0.000019	-2.08841
0.000010	0.000005	0.000002	0.000001	0.000001	0.000000	0.000000	0.000000	0.000000	0.000000	-1.45189
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	-0.08087
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	-0.10876
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	-0.55626
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.03139
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	-0.12116
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	-0.05413
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	-0.83486
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	-1.06148
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	-0.69641
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	-0.01406
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	-1.04083
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.609888
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	-0.24657

Predictor Variables										Dependent
V1	V2	V3	V4	V5	V6	V7	V8	V9	V10	Variable
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	-0.3763
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	-1.49206
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	-0.17637
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	-1.47338
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000001	-0.45066
0.000001	0.000002	0.000005	0.000010	0.000019	0.000036	0.000067	0.000123	0.000223	0.000394	-1.71334
0.000682	0.001159	0.001930	0.003151	0.005042	0.007907	0.012155	0.018316	0.027052	0.039164	-0.74203
0.055576	0.077305	0.105399	0.140858	0.184520	0.236928	0.298197	0.367879	0.444858	0.527292	-0.66797
0.612626	0.697676	0.778801	0.852144	0.913931	0.960789	0.990050	1.000000	0.990050	0.960789	-0.36114
0.913931	0.852144	0.778801	0.697676	0.612626	0.527292	0.444858	0.367879	0.298197	0.236928	-0.97318
0.184520	0.140858	0.105399	0.077305	0.055576	0.039164	0.027052	0.018316	0.012155	0.007907	-2.54985
0.005042	0.003151	0.001930	0.001159	0.000682	0.000394	0.000223	0.000123	0.000067	0.000036	-2.71749
0.000019	0.000010	0.000005	0.000002	0.000001	0.000001	0.000000	0.000000	0.000000	0.000000	-1.37393
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	-1.62491
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	-0.98101
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	-1.19692
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	-3.11507
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	-0.31209
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.237347
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	-0.72068
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	-0.53267
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	-1.14451
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.323257
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	-2.1319
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	1.188074
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	-1.18391
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	-1.27328
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	-1.40458
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	-0.60408
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	-1.35922
0.000001	0.000001	0.000002	0.000005	0.000010	0.000019	0.000036	0.000067	0.000123	0.000223	-0.45079
0.000394	0.000682	0.001159	0.001930	0.003151	0.005042	0.007907	0.012155	0.018316	0.027052	-1.29463
0.039164	0.055576	0.077305	0.105399	0.140858	0.184520	0.236928	0.298197	0.367879	0.444858	0.162774
0.527292	0.612626	0.697676	0.778801	0.852144	0.913931	0.960789	0.990050	1.000000	0.990050	-0.53674
0.960789	0.913931	0.852144	0.778801	0.697676	0.612626	0.527292	0.444858	0.367879	0.298197	-0.45683

Predictor Variables										Dependent
V1	V2	V3	V4	V5	V6	V7	V8	V9	V10	Variable
0.236928	0.184520	0.140858	0.105399	0.077305	0.055576	0.039164	0.027052	0.018316	0.012155	0.391253
0.007907	0.005042	0.003151	0.001930	0.001159	0.000682	0.000394	0.000223	0.000123	0.000067	0.117457
0.000036	0.000019	0.000010	0.000005	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	0.69869
1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	-1.85312
1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	-0.04861
1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	0.214684
1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	0.261316
1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	-0.57448
1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	2.468938
1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	-0.93785
1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.165921
1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	0.966748
1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	0.125721
1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	0.867138
1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	0.551458
1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	0.287231
1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	-0.75881
1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	0.551283
1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	0.066577
1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	0.503767
1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	0.067802
1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	-1.44586
1.000000	1.000000	1.000000	1.000000	1.000000	0.000000	0.000000	0.000001	0.000001	0.000002	0.884697
0.000005	0.000010	0.000019	0.000036	0.000067	0.000123	0.000223	0.000394	0.000682	0.001159	-0.49601
0.001930	0.003151	0.005042	0.007907	0.012155	0.018316	0.027052	0.039164	0.055576	0.077305	-0.24083
0.105399	0.140858	0.184520	0.236928	0.298197	0.367879	0.444858	0.527292	0.612626	0.697676	0.027056
0.778801	0.852144	0.913931	0.960789	0.990050	1.000000	0.990050	0.960789	0.913931	0.852144	0.189064
0.778801	0.697676	0.612626	0.527292	0.444858	0.367879	0.298197	0.236928	0.184520	0.140858	0.517325
0.105399	0.077305	0.055576	0.039164	0.027052	0.018316	0.012155	0.007907	0.005042	0.003151	1.688736
0.001930	0.001159	0.000682	0.000394	0.000223	0.000123	0.000067	0.000036	0.000019	0.000010	2.813648
0.000005	0.000002	0.000001	0.000001	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.877579
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	2.008548
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	1.728837
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	1.712295
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	2.676133

Predictor Variables										Dependent
V1	V2	V3	V4	V5	V6	V7	V8	V9	V10	Variable
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	2.522675
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	2.704179
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	2.171262
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	3.029813
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	3.048587
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	2.721537
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	2.74891
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	1.089289
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000001	0.000001	3.187072
0.000002	0.000005	0.000010	0.000019	0.000036	0.000067	0.000123	0.000223	0.000394	0.000682	3.197012
0.001159	0.001930	0.003151	0.005042	0.007907	0.012155	0.018316	0.027052	0.039164	0.055576	1.648355
0.077305	0.105399	0.140858	0.184520	0.236928	0.298197	0.367879	0.444858	0.527292	0.612626	1.283097
0.697676	0.778801	0.852144	0.913931	0.960789	0.990050	1.000000	0.990050	0.960789	0.913931	1.001207
0.852144	0.778801	0.697676	0.612626	0.527292	0.444858	0.367879	0.298197	0.236928	0.184520	2.190649
0.140858	0.105399	0.077305	0.055576	0.039164	0.027052	0.018316	0.012155	0.007907	0.005042	1.037059
0.003151	0.001930	0.001159	0.000682	0.000394	0.000223	0.000123	0.000067	0.000036	0.000019	0.617336
0.000010	0.000005	0.000002	0.000001	0.000001	0.000000	0.000000	0.000000	0.000000	0.000000	1.56651
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	-0.72404
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.015634
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	-1.2866
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.9474
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.804177
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	-1.07216
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.257943
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	-0.36585
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	-0.99646
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.360602
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	-0.72222
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.066804
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.379405
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.307738
0.000000	0.000000	0.000000	0.000000	0.000001	0.000001	0.000002	0.000005	0.000010	0.000019	-0.09646
0.000036	0.000067	0.000123	0.000223	0.000394	0.000682	0.001159	0.001930	0.003151	0.005042	-0.59666
0.007907	0.012155	0.018316	0.027052	0.039164	0.055576	0.077305	0.105399	0.140858	0.184520	-0.07479
0.236928	0.298197	0.367879	0.444858	0.527292	0.612626	0.697676	0.778801	0.852144	0.913931	0.366227

Predictor Variables										Dependent
V1	V2	V3	V4	V5	V6	V7	V8	V9	V10	Variable
0.960789	0.990050	1.000000	0.990050	0.960789	0.913931	0.852144	0.778801	0.697676	0.612626	0.146715
0.527292	0.444858	0.367879	0.298197	0.236928	0.184520	0.140858	0.105399	0.077305	0.055576	-1.03773
0.039164	0.027052	0.018316	0.012155	0.007907	0.005042	0.003151	0.001930	0.001159	0.000682	0.43298
0.000394	0.000223	0.000123	0.000067	0.000036	0.000019	0.000010	0.000005	0.000002	0.000001	-0.77253
0.000001	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	-1.59873
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	-0.91667
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	-0.18372
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.05454
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	-1.29388
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	-1.58155
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	-2.46637
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	-2.70749
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	-2.9947
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	-2.85241
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	-2.46247
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	-3.73826
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	-3.68025
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	-3.57917
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	-3.69291
0.000000	0.000000	0.000000	0.000000	0.000000	0.000001	0.000001	0.000002	0.000005	0.000010	-3.69046
0.000019	0.000036	0.000067	0.000123	0.000223	0.000394	0.000682	0.001159	0.001930	0.003151	-2.85299
0.005042	0.007907	0.012155	0.018316	0.027052	0.039164	0.055576	0.077305	0.105399	0.140858	-4.54066
0.184520	0.236928	0.298197	0.367879	0.444858	0.527292	0.612626	0.697676	0.778801	0.852144	-3.46635
0.913931	0.960789	0.990050	1.000000	0.990050	0.960789	0.913931	0.852144	0.778801	0.697676	-2.3129
0.612626	0.527292	0.444858	0.367879	0.298197	0.236928	0.184520	0.140858	0.105399	0.077305	-1.909
0.055576	0.039164	0.027052	0.018316	0.012155	0.007907	0.005042	0.003151	0.001930	0.001159	-1.38891
0.000682	0.000394	0.000223	0.000123	0.000067	0.000036	0.000019	0.000010	0.000005	0.000002	-1.70557
0.000001	0.000001	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	-2.08043
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	-1.34632
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	-1.84107
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	-1.83476
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	-0.86864
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	-0.65575
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.340095
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	-1.0628

Predictor Variables										Dependent
V1	V2	V3	V4	V5	V6	V7	V8	V9	V10	Variable
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	1.159148
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	1.126134
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	-0.15135
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	-0.57837
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	1.241583
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	1.165105
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	-0.2
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	-0.23279
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	1.092664
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	-0.52286
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	1.348673
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	-0.22802
0.000000	0.000001	0.000001	0.000002	0.000005	0.000010	0.000019	0.000036	0.000067	0.000123	0.260234
0.000223	0.000394	0.000682	0.001159	0.001930	0.003151	0.005042	0.007907	0.012155	0.018316	1.027092
0.027052	0.039164	0.055576	0.077305	0.105399	0.140858	0.184520	0.236928	0.298197	0.367879	0.585037
0.444858	0.527292	0.612626	0.697676	0.778801	0.852144	0.913931	0.960789	0.990050	1.000000	-0.5898
0.990050	0.960789	0.913931	0.852144	0.778801	0.697676	0.612626	0.527292	0.444858	0.367879	0.439033
0.298197	0.236928	0.184520	0.140858	0.105399	0.077305	0.055576	0.039164	0.027052	0.018316	-0.42928

Table 8: Gene Expression Data and Survival for 50 Genes from Alizadeh et al

Patient	Survival Time	Outcome	X1554	X1639	X1777	X1876	X1908	X1940	X2045	X2208	X2339	X2383	X2395	X2430	X2491
V32	1.3	1	0.270	-0.730	-0.100	-0.080	0.570	-0.510	0.520	1.830	0.500	0.110	-0.630	-0.250	1.940
V17	2.4	1	-0.170	-0.480	-0.560	-0.470	-0.350	0.860	0.830	2.320	-0.080	0.770	-0.740	-0.230	0.220
V18	2.9	1	0.040	-0.010	-1.110	-0.880	-0.540	-0.340	0.380	2.730	0.580	0.300	-0.580	0.120	1.390
V6	3.2	1	-0.300	0.020	-0.440	-0.300	-0.220	-0.140	1.430	0.640	0.100	0.370	-0.480	-0.530	0.110
V2	3.4	1	-0.050	-0.096	-0.700	-0.390	-0.140	-0.140	0.540	-0.230	0.090	1.130	0.090	0.000	0.480
V12	4.1	1	-0.050	-0.200	0.570	-0.190	0.360	0.400	0.040	0.000	-0.120	-0.190	0.270	0.090	-0.530
V20	4.6	1	-0.360	1.100	-0.620	-0.520	-0.160	-0.290	0.570	0.900	0.460	0.100	-0.520	0.000	-0.180
V25	5.1	1	-0.010	-0.300	-0.410	-1.070	0.160	-0.410	0.620	1.860	0.020	0.500	0.050	0.050	1.720

Patient	Survival Time	Outcome	X1554	X1639	X1777	X1876	X1908	X1940	X2045	X2208	X2339	X2383	X2395	X2430	X2491
V21	8.2	1	-0.810	-0.295	-1.190	-0.434	-0.330	-0.640	-0.470	-0.480	-0.250	-0.209	-0.148	-0.290	0.220
V7	8.3	1	-0.230	-0.750	0.320	-0.260	0.220	-0.270	0.750	0.540	0.440	-0.620	0.260	-0.050	0.640
V39	9.5	1	-0.250	0.370	-0.340	0.980	-0.380	-0.370	-3.210	2.470	0.930	-0.220	-0.770	0.650	-0.920
V24	11.8	1	0.000	-0.140	-0.460	-0.340	-0.170	0.000	0.310	0.630	-0.020	0.000	0.270	0.660	1.000
V29	12.3	1	0.390	-0.360	0.120	-0.240	0.180	0.890	-1.180	0.600	-0.080	-0.870	0.480	-0.310	0.930
V33	12.7	1	0.260	0.060	-0.040	0.150	0.190	0.800	-0.310	0.290	0.170	-0.170	-0.370	-0.130	0.260
V16	15.5	1	-0.290	-0.210	-0.660	-0.980	-0.030	0.340	0.350	-0.620	0.630	0.380	-0.160	0.280	0.080
V40	22.3	1	-0.150	-0.380	-0.080	-0.500	-0.090	-0.220	-0.760	1.670	-0.490	-0.009	0.550	-0.400	-0.290
V13	23.7	1	-0.920	-0.460	-1.150	-0.380	-0.440	0.460	-0.660	0.700	0.790	0.220	0.000	-0.270	0.070
V11	27.1	1	0.060	-1.620	-0.590	-0.340	-0.080	-1.300	0.890	1.450	-0.080	-0.025	-1.080	-0.560	1.620
V37	31.5	1	-0.090	0.050	-0.290	-0.230	0.070	-0.820	0.740	1.190	-0.340	0.370	0.760	0.610	0.640
V23	32.5	1	-0.380	0.060	-0.150	-0.570	0.120	-0.470	-0.530	0.250	-0.480	-0.390	0.390	0.320	0.700
V38	39.6	1	-0.145	0.060	0.340	-0.270	1.240	0.280	-1.320	-2.580	0.180	-0.040	0.510	-0.040	-1.570
V5	51.2	0	-0.070	-0.380	-0.080	0.000	0.130	0.050	0.190	0.130	0.220	-0.760	0.190	-0.110	0.190
V36	53.7	0	-0.200	-0.410	-0.320	-0.430	-0.600	0.240	2.170	0.350	0.310	-0.050	-0.320	0.370	-0.090
V15	56.6	0	-0.820	0.160	-0.040	-1.250	0.500	-0.550	-0.380	-0.010	-0.760	0.460	0.110	0.200	0.790
V14	59.0	0	-0.340	-0.043	-0.700	-0.056	0.198	1.000	0.630	0.290	0.000	0.298	-0.090	0.120	-0.060
V31	68.8	0	0.080	-0.140	0.200	0.110	-0.080	0.160	0.230	1.330	0.290	-0.250	-0.050	-0.050	0.430
V30	69.1	0	0.380	0.720	0.700	0.390	0.000	-0.580	-0.670	-0.480	-0.610	-0.640	0.440	1.630	0.590
V4	69.6	0	-0.060	-0.570	-0.380	-0.830	0.060	-0.010	0.470	1.230	0.010	-0.060	0.210	-0.090	0.150
V3	71.3	1	-0.400	-0.280	-0.390	-0.490	-0.040	-0.080	1.640	2.110	0.220	-0.100	0.210	0.010	-0.700
V28	71.3	0	0.700	0.160	0.100	0.160	0.310	0.260	0.650	0.720	-0.290	-1.200	0.630	-0.140	0.370
V34	72.0	0	-0.940	-0.050	-0.060	-0.240	-0.070	0.440	-1.500	0.170	0.090	0.147	-0.050	0.340	3.630
V1	77.4	0	0.000	0.530	0.980	0.380	0.910	1.080	3.210	2.580	-0.220	-0.140	-0.870	0.100	-0.970
V19	80.4	0	-0.190	-0.340	-0.950	-0.430	-0.410	0.150	-0.110	-0.800	-0.050	-0.870	-0.780	-0.100	0.170
V27	83.8	0	0.280	0.000	-1.110	-1.040	-0.570	-0.150	0.720	1.080	0.070	0.220	-0.180	0.620	0.000
V10	88.1	0	0.690	-0.370	0.000	0.130	0.060	-0.160	0.670	-0.910	0.120	-0.130	-0.590	0.220	-0.600
V9	89.8	0	-0.220	-0.700	-0.790	-0.340	-0.260	0.190	-1.130	-1.960	-0.150	0.490	0.540	0.320	0.710
V26	90.2	0	-0.200	0.420	-0.270	0.240	0.470	-0.670	-0.280	0.380	-0.890	0.850	0.000	-0.210	-0.440
V35	91.3	0	-0.560	-0.660	-0.810	-0.530	-0.250	-0.250	0.720	-1.160	0.230	0.090	-0.350	0.940	0.720
V8	102.4	0	0.260	-0.800	0.420	0.260	-0.030	0.450	-0.870	0.550	0.380	0.280	0.120	0.170	0.260
V22	129.9	0	-0.680	-0.120	-0.210	-0.460	0.690	-0.390	0.070	0.490	-0.670	0.910	-0.220	-0.150	1.200

Patient	Survival Time	Outcome	X2544	X2640	X2824	X2882	X2922	X3041	X3138	X3171	X3249	X3346	X3494	X4021
V32	1.3	1	-0.110	0.280	-0.120	0.560	1.440	-0.300	0.440	2.470	-0.230	-0.150	0.300	0.090
V17	2.4	1	0.050	-0.150	0.050	-0.260	0.610	0.050	0.070	1.490	-0.370	0.060	0.180	0.010
V18	2.9	1	0.380	2.030	1.740	1.050	0.080	1.480	0.840	0.000	0.570	1.110	0.035	-0.620
V6	3.2	1	-0.480	-0.180	-0.220	-0.270	-0.770	0.180	-0.410	1.520	-0.820	0.670	0.040	-0.190
V2	3.4	1	-0.120	-0.260	-0.510	0.240	-0.250	0.220	0.290	0.670	0.340	-0.280	-0.080	0.240
V12	4.1	1	-0.210	-0.160	-0.960	-0.450	0.620	-0.330	0.210	0.860	-0.340	-0.310	-0.310	1.640
V20	4.6	1	0.010	-0.120	-0.480	-0.130	0.400	-0.060	-0.070	0.470	-0.250	-0.090	0.040	-0.160
V25	5.1	1	-0.520	-0.530	0.070	-1.010	-2.590	-0.480	-0.030	2.010	-0.990	0.810	0.890	-0.180
V21	8.2	1	0.150	-0.100	0.250	0.400	-0.340	0.820	0.520	0.990	-0.120	0.600	-0.440	0.610
V7	8.3	1	-0.250	-0.090	0.060	0.240	-0.260	-0.230	0.130	1.040	0.440	-0.440	-0.200	0.030
V39	9.5	1	-0.060	0.630	0.510	0.890	0.410	0.280	0.000	1.040	0.380	-1.210	0.630	0.290
V24	11.8	1	-0.660	0.350	0.140	-0.140	-0.630	0.070	-0.350	1.280	0.260	0.420	0.310	-0.030
V29	12.3	1	0.010	0.030	0.070	0.000	0.530	0.090	0.240	1.360	-0.240	-0.050	0.000	0.100
V33	12.7	1	0.120	-0.250	0.040	-0.220	0.720	0.110	-0.100	1.540	-0.270	0.500	-0.260	0.550
V16	15.5	1	-0.290	-0.510	0.570	0.140	-1.020	-0.080	-0.030	0.090	0.360	0.460	0.190	-0.300
V40	22.3	1	-0.130	0.010	0.150	0.590	0.970	0.440	-0.160	1.480	0.530	-0.280	-0.450	1.080
V13	23.7	1	-0.470	0.120	0.590	0.260	0.570	0.550	0.133	-0.950	-0.280	0.010	0.140	-0.007
V11	27.1	1	0.560	0.700	0.400	0.780	0.040	0.010	0.330	-0.130	0.230	-0.070	0.980	-0.560
V37	31.5	1	-0.130	1.090	0.880	0.910	0.060	0.350	0.170	0.750	-0.200	-0.460	-0.470	-0.340
V23	32.5	1	-0.290	0.000	0.360	-0.560	-1.180	0.020	0.170	0.710	-0.740	0.330	0.180	-0.300
V38	39.6	1	0.040	0.220	0.880	-0.250	-1.150	0.380	0.250	-0.160	-0.410	-0.110	0.380	-0.620
V5	51.2	0	-0.051	0.460	0.210	0.390	0.260	0.280	0.270	1.830	0.030	-0.040	-0.700	-0.080
V36	53.7	0	0.110	0.140	-0.310	-0.160	0.040	-0.160	-0.150	-0.520	-0.180	0.130	0.100	-1.410
V15	56.6	0	-0.460	0.160	0.030	-0.340	1.000	0.170	0.360	-0.820	-0.310	0.420	0.280	0.240
V14	59.0	0	0.110	-0.250	-0.150	0.040	0.030	0.180	0.040	-0.470	-0.280	-0.050	0.268	-0.310
V31	68.8	0	-0.140	0.010	0.000	0.350	0.890	-0.010	0.000	0.880	-0.170	-0.090	-0.400	0.060
V30	69.1	0	-0.670	0.240	0.450	1.240	1.180	-0.110	-0.080	-0.080	-0.210	0.010	-0.790	0.280
V4	69.6	0	0.130	0.380	0.480	0.450	0.920	0.250	0.100	-0.790	0.420	0.290	-0.300	-0.090
V3	71.3	1	-0.070	0.470	-0.090	0.140	-0.320	0.250	0.790	0.040	0.100	0.010	-0.890	-0.610
V28	71.3	0	-0.580	-0.240	-0.010	-0.050	0.200	0.080	-0.210	0.770	0.000	-0.010	0.060	0.090
V34	72.0	0	-0.280	0.120	0.690	0.120	-0.080	0.260	0.210	2.460	0.220	-0.440	0.170	-0.640
V1	77.4	0	-0.110	0.130	-1.610	-1.150	0.550	-0.420	0.230	-1.190	-0.010	0.180	-0.390	-0.810
V19	80.4	0	0.000	0.360	0.890	0.710	0.530	0.370	0.230	0.440	0.510	0.710	-0.590	-0.540
V27	83.8	0	-0.020	0.590	0.580	0.630	0.310	0.160	-0.070	0.700	-0.240	0.380	0.140	-0.500

Patient	Survival Time	Outcome	X2544	X2640	X2824	X2882	X2922	X3041	X3138	X3171	X3249	X3346	X3494	X4021
V10	88.1	0	0.080	-0.590	-0.570	-0.410	-0.100	-0.290	-0.490	-0.270	-0.730	0.320	-0.180	-0.330
V9	89.8	0	0.110	0.250	0.600	0.760	-0.020	0.770	0.300	-0.610	0.750	-0.350	-0.300	0.640
V26	90.2	0	-0.140	-0.250	0.120	-0.380	-0.160	0.010	-0.030	0.170	-0.540	0.520	0.840	0.730
V35	91.3	0	-0.550	1.050	1.290	0.700	0.180	0.290	0.790	0.450	-0.660	0.090	-0.380	-0.180
V8	102.4	0	0.200	0.340	1.620	1.350	1.550	0.210	0.440	1.050	0.030	-0.530	-0.090	0.490
V22	129.9	0	-0.210	-0.330	0.300	-0.210	-0.190	-0.200	-0.160	1.630	-0.540	0.000	0.500	-0.030

			Gene											
Patient	Survival Time	Outcome	X9	X206	X234	X281	X286	X388	X396	X456	X482	X690	X827	X1075	X1098
V32	1.3	1	-1.110	-0.150	0.920	0.000	0.520	-0.140	-0.440	0.250	0.510	-0.260	-0.120	1.340	-0.710
V17	2.4	1	-0.520	-0.100	1.580	0.580	0.270	-0.040	-0.040	1.040	0.170	-0.860	0.260	-1.320	0.290
V18	2.9	1	0.350	1.000	0.010	3.840	0.450	0.880	0.640	0.510	-0.740	-0.890	-1.080	-0.160	0.130
V6	3.2	1	0.390	0.130	-0.140	-0.830	-0.330	0.430	-0.580	0.030	0.120	-0.700	-0.880	0.960	0.200
V2	3.4	1	0.110	0.100	2.100	0.370	-0.090	0.690	0.520	0.530	0.170	0.660	-0.360	0.910	-0.013
V12	4.1	1	-1.020	-0.070	0.810	-0.010	0.310	0.440	0.850	0.330	-0.020	0.380	0.160	-0.790	-0.350
V20	4.6	1	-0.070	0.030	1.460	0.670	0.060	0.560	0.800	0.270	0.150	-0.910	-0.550	-0.410	-0.140
V25	5.1	1	0.410	0.230	0.340	0.050	-0.910	-0.300	-0.820	0.350	-0.460	-0.330	-1.810	0.880	-0.800
V21	8.2	1	-0.690	-0.060	1.140	1.800	0.270	-1.190	-1.420	0.090	-0.350	-0.405	-0.400	-0.290	1.910
V7	8.3	1	-0.380	-0.110	0.190	0.110	0.000	0.210	-0.110	0.300	-0.070	0.630	0.030	-1.280	-0.160
V39	9.5	1	-0.490	0.340	-0.420	0.650	0.970	1.170	1.030	0.530	-1.200	1.330	0.000	-0.950	-0.060
V24	11.8	1	0.460	0.330	0.080	1.770	0.950	-0.100	-0.040	-0.090	-0.140	-0.470	-0.210	-0.900	-0.040
V29	12.3	1	0.250	0.050	0.520	-1.160	-0.420	0.180	0.510	0.090	-0.100	0.580	0.360	-0.140	-1.180
V33	12.7	1	-1.150	0.000	1.340	0.590	0.400	-2.140	-1.880	0.410	0.020	-0.960	-0.140	-1.710	-0.460
V16	15.5	1	0.280	-0.140	0.500	-2.220	-1.220	-0.200	-0.910	-0.940	-0.610	-1.010	0.160	0.190	-0.680
V40	22.3	1	0.100	-0.090	0.120	-0.030	-1.080	-0.600	-0.750	0.450	-0.160	-0.570	0.130	0.210	-0.243
V13	23.7	1	0.070	0.180	0.850	1.270	0.200	0.570	-1.170	-0.330	0.090	-1.390	-0.340	-1.010	-0.030
V11	27.1	1	-0.340	0.260	-0.110	-0.850	-0.740	0.440	-1.750	-0.640	0.900	-0.680	-0.790	0.280	-0.560
V37	31.5	1	0.380	0.310	0.630	2.760	1.750	0.220	-0.310	0.030	0.100	-0.120	0.140	-1.220	-0.030
V23	32.5	1	0.230	-0.180	-0.040	-0.640	-1.100	-0.990	-0.980	-0.270	-0.690	-0.790	-0.580	-0.850	-0.220
V38	39.6	1	0.220	0.050	0.000	-2.080	-0.930	0.630	-1.590	-0.290	0.000	-1.280	0.540	0.570	-0.070
V5	51.2	0	0.150	0.050	-2.480	1.260	0.680	0.730	1.020	0.220	0.480	0.020	0.340	-0.780	-0.210
V36	53.7	0	0.370	0.430	0.600	0.700	0.580	1.510	0.540	0.130	0.320	0.380	-0.260	-0.430	-0.100
V15	56.6	0	0.880	0.440	-0.050	1.350	0.560	-2.360	-1.070	0.300	-0.300	0.320	0.450	-1.580	-0.040
V14	59.0	0	-0.450	-0.190	0.020	0.010	-0.460	-1.300	0.020	0.100	-0.350	0.820	-0.280	-0.730	0.071

			Gene												
	Survival														
Patient	Time	Outcome	X9	X206	X234	X281	X286	X388	X396	X456	X482	X690	X827	X1075	X1098
V31	68.8	0	-1.090	-0.210	0.450	-0.090	0.170	0.400	0.640	0.470	-0.330	-0.810	0.080	-0.510	-0.420
V30	69.1	0	-0.610	-0.130	-0.180	0.390	0.110	0.030	0.720	0.070	-0.290	0.000	0.730	-1.140	0.180
V4	69.6	0	0.100	0.360	-0.690	0.590	-0.120	0.280	-0.280	-0.090	0.350	-0.100	-0.130	0.180	-0.110
V3	71.3	1	-0.250	0.390	-0.150	-0.250	-0.470	-1.630	0.350	0.360	0.560	0.730	-0.290	-1.060	0.080
V28	71.3	0	-0.160	0.000	0.290	0.160	0.260	0.130	0.400	0.040	-0.500	-0.550	0.190	-1.530	-0.490
V34	72.0	0	-0.400	-0.100	-0.210	0.490	0.460	0.500	-0.260	-0.360	-0.270	-1.580	-0.890	-0.870	0.850
V1	77.4	0	0.390	-0.990	-1.750	-2.460	-0.127	-1.240	-1.240	-1.190	0.380	-1.060	0.140	-0.980	0.660
V19	80.4	0	0.000	0.520	0.550	-0.230	-0.490	0.520	-0.440	-0.100	0.460	0.680	-0.410	0.730	-0.310
V27	83.8	0	-0.660	0.540	0.490	1.890	0.800	0.110	0.320	-0.210	-0.440	-1.340	-1.390	-0.090	-0.490
V10	88.1	0	-0.260	-0.230	-0.670	-0.490	0.030	0.200	0.000	0.370	0.330	0.660	-0.090	0.520	0.140
V9	89.8	0	0.170	-0.280	0.540	-0.270	-0.440	0.100	-0.320	-0.040	0.760	-1.430	-0.240	0.980	-0.446
V26	90.2	0	-0.030	-0.350	-0.070	-0.870	-0.610	-0.660	-0.170	-0.380	-0.320	-0.640	-0.380	-1.310	-0.146
V35	91.3	0	0.750	0.220	-1.840	0.040	0.540	0.810	0.440	0.430	0.370	-0.760	-0.530	0.760	-0.270
V8	102.4	0	-0.300	0.020	-0.590	0.370	0.160	-1.390	1.140	0.090	0.110	0.040	-0.030	0.040	-0.050
V22	129.9	0	-0.110	-0.190	0.040	-0.370	-0.810	-0.250	0.000	-0.190	-1.200	-0.500	-1.000	0.370	-0.150

	Survival												
Patient	Time	Outcome	X1100	X1108	X1130	X1135	X1182	X1202	X1245	X1341	X1350	X1421	X1441	X1535
V32	1.3	1	-0.150	0.000	-1.070	-0.050	1.420	0.010	-1.400	0.110	0.310	-0.470	0.080	0.630
V17	2.4	1	-0.460	-0.010	0.120	0.690	1.740	0.260	-2.750	1.260	0.440	-0.380	0.150	0.130
V18	2.9	1	-1.120	0.030	-0.410	-0.210	0.344	-0.390	-2.140	-1.360	0.050	0.560	0.100	-0.340
V6	3.2	1	0.280	-0.150	0.400	0.010	-0.120	0.090	-1.360	-1.040	0.104	-0.550	0.420	-0.050
V2	3.4	1	0.004	-0.210	-0.240	0.140	0.430	0.580	0.060	1.380	0.230	0.470	-0.370	0.340
V12	4.1	1	-0.070	-0.310	-0.250	0.520	0.080	0.950	-0.690	0.380	-0.330	-0.620	0.110	0.310
V20	4.6	1	-0.780	0.180	1.120	1.240	0.900	0.170	0.070	1.680	0.080	-0.470	-0.170	0.100
V25	5.1	1	0.920	0.270	0.300	0.730	0.910	-0.250	-0.360	-0.030	0.910	-0.030	-0.200	-0.720
V21	8.2	1	-0.145	-0.580	-1.190	-0.630	-0.590	-0.006	-0.224	0.205	0.190	0.130	-0.110	-1.220
V7	8.3	1	-0.310	0.090	0.350	0.460	0.480	0.160	0.320	0.630	-0.170	-0.010	0.060	0.250
V39	9.5	1	-0.290	-0.040	1.170	0.800	-0.570	-0.050	-0.166	-0.840	-0.720	-0.120	-0.150	0.160
V24	11.8	1	0.110	0.040	0.890	1.210	-0.090	-0.620	0.030	0.190	0.140	0.130	-0.190	0.080
V29	12.3	1	-0.250	-0.070	-0.280	0.240	0.090	0.240	0.950	1.420	0.160	-0.340	0.000	-0.060
V33	12.7	1	0.080	-0.110	-1.560	-0.410	0.290	-0.240	-0.150	2.090	0.480	0.340	-0.730	0.070
V16	15.5	1	-0.120	0.200	-0.600	-0.430	1.560	-0.140	-0.970	0.970	0.570	0.240	-0.110	-0.480
V40	22.3	1	-0.310	-0.220	0.140	0.110	0.220	0.790	-0.050	-0.210	-0.220	-0.960	0.070	-0.330

Patient	Survival Time	Outcome	X1100	X1108	X1130	X1135	X1182	X1202	X1245	X1341	X1350	X1421	X1441	X1535
V13	23.7	1	0.130	0.020	0.460	0.230	0.380	-0.570	-0.370	-1.550	0.480	0.070	0.090	-0.160
V11	27.1	1	-0.950	-0.370	-0.960	-0.110	0.390	0.120	-1.170	1.230	0.530	-0.100	-0.250	-0.420
V37	31.5	1	-0.160	-1.070	-1.200	-0.690	-0.500	-0.190	0.370	-0.360	0.119	0.120	-0.150	0.630
V23	32.5	1	0.180	-0.030	0.530	0.700	-0.010	-0.540	1.480	-0.870	0.280	0.270	-0.220	-0.310
V38	39.6	1	0.160	0.400	0.760	0.450	0.440	-0.510	0.150	-2.250	0.140	0.320	-0.570	0.010
V5	51.2	0	-0.070	-0.380	-0.730	-0.070	-0.090	0.060	0.890	-0.410	0.375	0.050	-0.120	0.370
V36	53.7	0	-0.380	-0.260	0.410	0.620	-0.560	-0.010	-0.240	0.330	0.130	-0.360	0.400	0.080
V15	56.6	0	0.200	-0.180	-1.060	-0.590	-0.230	-0.900	-0.620	0.223	-0.060	-0.540	0.100	-0.210
V14	59.0	0	0.250	0.550	-0.087	0.373	0.510	0.190	0.110	0.334	-0.010	0.990	0.500	-0.150
V31	68.8	0	0.200	-0.110	-0.680	0.000	0.210	0.280	-0.140	1.230	0.130	-0.460	-0.190	0.080
V30	69.1	0	0.380	-0.410	0.010	0.500	0.000	0.010	0.960	-0.320	-0.240	-0.530	0.180	0.410
V4	69.6	0	-0.340	-0.380	-1.040	-0.220	-0.350	0.480	0.860	0.680	0.220	0.330	-0.200	0.170
V3	71.3	1	-0.360	0.170	-0.450	0.070	-0.110	0.110	-1.220	0.150	0.190	-0.270	0.440	0.100
V28	71.3	0	0.210	-0.100	0.130	0.440	0.160	0.390	1.170	0.790	0.200	0.110	-0.260	0.130
V34	72.0	0	0.510	0.610	-0.150	0.320	0.500	0.430	0.760	-0.340	0.270	0.150	-0.460	0.220
V1	77.4	0	0.120	-0.430	-0.990	-0.170	0.600	0.220	-1.590	0.300	-0.370	-0.250	-0.180	-0.610
V19	80.4	0	-0.170	0.300	-0.390	0.170	0.280	-0.950	-0.370	0.550	0.780	0.410	-0.350	-0.570
V27	83.8	0	0.300	-0.010	-0.240	0.000	-0.930	-0.530	-0.410	0.170	0.470	0.420	0.020	-1.430
V10	88.1	0	-0.080	-0.050	0.170	0.040	0.560	0.670	-0.070	-0.060	-0.200	-0.250	0.110	0.010
V9	89.8	0	0.000	-0.240	-1.080	-0.410	0.270	0.220	0.680	1.740	0.130	0.190	-0.580	-0.050
V26	90.2	0	-0.041	0.360	0.190	0.310	0.660	0.070	2.990	-0.370	0.270	-1.000	0.080	0.000
V35	91.3	0	-0.240	-0.370	-0.800	-0.350	0.900	0.190	0.920	0.650	0.137	0.740	0.070	-0.110
V8	102.4	0	-0.550	-0.540	0.210	0.450	-0.480	0.630	1.450	0.080	-1.080	-0.040	-0.030	0.000
V22	129.9	0	0.350	-0.030	-0.400	-0.100	0.800	0.220	0.890	-0.400	0.380	-0.140	-0.030	-0.310

Example 6: Lymphoma Survival Analysis

This example uses real survival data from http://llmpp.nih.gov/lymphoma/data.shtml

The companion article is Alizadeh AA, et al. (2000) Distinct types of diffuse large B-cell lymphoma

identified by gene expression profiling. Nature 403(6769):503-11

The data is microarray data consisting of data for 4026 genes and 40 samples (individuals) with survival times and censor indicator available for each sample. The results were analysed using the algorithm, implementing a Cox's proportional hazards model.

Note that the algorithm has selected 3 genes as being associated with survival time (gene: 3797X, 3302X, 356X).

Example 7: Reduced Lymphoma Survival Analysis

For completeness of documentation, we also present an example based on a subset of the genes from Alizadeh et al. 50 genes were selected, including 47 chosen at random and 3 genes identified as significant in the analysis of the full data set. The data are shown in the following table 9, which gives gene expression (for the reduced set of 50 genes), and survival for each patient.

The data were analysed using the version of the algorithm containing Cox's proportional hazard survival model. After 22 iterations, five genes were selected, including 2 genes from the solution for the full set. The full results (including an iteration history) are given below:

```
**************************************************
EM Iteration:  0 expected post:  2
**************************************************
Number of basis functions 50

**************************************************
EM Iteration:  1 expected post:  -56.0195287084271
**************************************************
Number of basis functions 50
```

```
**************************************************
EM Iteration:  2 expected post:  -54.947811363042
**************************************************
Number of basis functions 37

**************************************************
EM Iteration:  3 expected post:  -54.3317631914479
**************************************************
Number of basis functions 21

**************************************************
EM Iteration:  4 expected post:  -54.0607159790051
**************************************************
Number of basis functions 13

**************************************************
EM Iteration:  5 expected post:  -53.7980836894172
**************************************************
Number of basis functions 10
ID(s) of the variable(s) left in model
3 4 14 16 17 20 25 33 43 50
regression coefficients
1.30171200916394 1.48405810198456e-005 -0.491799506481601
0.688155245054059 5.82517870544154e-007 -1.13172255995036
2.95075622492565e-008 0.000301721699857512
-0.748378079168908 1.2775730496471

**************************************************

**************************************************
EM Iteration:  6 expected post:  -53.5560385409619
**************************************************
Number of basis functions 8
ID(s) of the variable(s) left in model
```

```
3 4 14 16 20 33 43 50
regression coefficients
1.30877141820174 1.11497455349489e-009 -0.440934673358609
0.731610034191797 -1.15246816508172 8.10391142899109e-007
-0.736752926831824 1.29017005214433

**************************************************

**************************************************
EM Iteration:  7 expected post:  -53.4357726710363
**************************************************
Number of basis functions 6
ID(s) of the variable(s) left in model
3 14 16 20 43 50
regression coefficients
1.30981441669383 -0.377350760745259 0.751065294832691
-1.16718699172136 -0.722720884604726 1.29171119706608

**************************************************

**************************************************
EM Iteration:  8 expected post:  -53.4338660629788
**************************************************
Number of basis functions 6
ID(s) of the variable(s) left in model
3 14 16 20 43 50
regression coefficients
1.30685231664004 -0.29722933884524 0.758547724825121
-1.17959350866281 -0.703886124955911 1.28487528071873

**************************************************

**************************************************
EM Iteration:  9 expected post:  -53.5154485460488
```

```
**************************************************
Number of basis functions 6
ID(s) of the variable(s) left in model
3 14 16 20 43 50
regression coefficients
1.30125961104666 -0.199901821555315 0.760639983868042
-1.19192749808285 -0.679917691918485 1.27242335041331

**************************************************

**************************************************
EM Iteration:  10 expected post:  -53.6545745873571
**************************************************
Number of basis functions 6
ID(s) of the variable(s) left in model
3 14 16 20 43 50
regression coefficients
1.29433188361771 -0.0976106309061782 0.760491979596701
-1.20394672329711 -0.653272803573524 1.25725914248418

**************************************************

**************************************************
EM Iteration:  11 expected post:  -53.820846021012
**************************************************
Number of basis functions 6
ID(s) of the variable(s) left in model
3 14 16 20 43 50
regression coefficients
1.28789874198243 -0.0244121499875095 0.759681966852181
-1.21216963682011 -0.630795741658714 1.24350708784212

**************************************************
```

```
**************************************************
EM Iteration:  12 expected post:  -53.9601661781558
**************************************************
Number of basis functions 6
ID(s) of the variable(s) left in model
3 14 16 20 43 50
regression coefficients
1.28354595931721 -0.00154101225658052 0.758893058476497
-1.21415984287542 -0.618231410989467 1.2344850269793

**************************************************

**************************************************
EM Iteration:  13 expected post:  -54.0328345444009
**************************************************
Number of basis functions 6
ID(s) of the variable(s) left in model
3 14 16 20 43 50
regression coefficients
1.2812179536199 -6.11852419349075e-006 0.75822352070402
-1.2134621579905 -0.612781276468739 1.22967591873953

**************************************************

**************************************************
EM Iteration:  14 expected post:  -54.06432139112
**************************************************
Number of basis functions 5
ID(s) of the variable(s) left in model
3 16 20 43 50
regression coefficients
1.28009759620513 0.757715617722854 -1.21278912622521
-0.610380879961096 1.22727470412141
```

```
**************************************************

**************************************************
EM Iteration:  15 expected post:  -54.0802180622945
**************************************************
Number of basis functions 5
ID(s) of the variable(s) left in model
3 16 20 43 50
regression coefficients
1.27956525855826 0.757384281713778 -1.21240801636852
-0.609289206977176 1.22609802569321

**************************************************

**************************************************
EM Iteration:  16 expected post:  -54.0881669099217
**************************************************
Number of basis functions 5
ID(s) of the variable(s) left in model
3 16 20 43 50
regression coefficients
1.27931094048991 0.75718874424491 -1.21221126091477
-0.608784296852685 1.22552534756029

**************************************************

**************************************************
EM Iteration:  17 expected post:  -54.0920771115648
**************************************************
Number of basis functions 5
ID(s) of the variable(s) left in model
3 16 20 43 50
regression coefficients
1.27918872576943 0.757080124746806 -1.21211237581804
```

```
-0.608548335650073 1.22524731506564

**************************************************

**************************************************
EM Iteration:  18 expected post:  -54.0939910705254
**************************************************
Number of basis functions 5
ID(s) of the variable(s) left in model
3 16 20 43 50
regression coefficients
1.27912977236735 0.757022055016955 -1.2120632265046
-0.608437260261357 1.22511245075764

**************************************************

**************************************************
EM Iteration:  19 expected post:  -54.0949258560397
**************************************************
Number of basis functions 5
ID(s) of the variable(s) left in model
3 16 20 43 50
regression coefficients
1.27910127561155 0.7569917935789 -1.2120389492013
-0.608384684306891 1.22504705594823

**************************************************

**************************************************
EM Iteration:  20 expected post:  -54.0953817354683
**************************************************
Number of basis functions 5
ID(s) of the variable(s) left in model
3 16 20 43 50
```

```
regression coefficients
1.27908748612817 0.756976302198781 -1.21202700813484
-0.608359689289364 1.22501535228942

**************************************************

**************************************************
EM Iteration:  21 expected post:  -54.0956037952427
**************************************************
Number of basis functions 5
ID(s) of the variable(s) left in model
3 16 20 43 50
regression coefficients
1.27908080980647 0.756968473084121 -1.21202115330035
-0.608347764395965 1.2249999841173

**************************************************

**************************************************
EM Iteration:  22 expected post:  -54.0957118531261
**************************************************
Number of basis functions 5
ID(s) of the variable(s) left in model
3 16 20 43 50
regression coefficients
1.27907757649105 0.756964553746695 -1.21201828961347
-0.608342058719735 1.2249925351853
```

Example 8: Survival Analysis with a parametric hazard

The data is 1694w.dat from http://www.wpi.edu/~mhchen/survbook/. This is data on survival of melanoma. There are n=255 individuals, 100 of whom have censored survival times. Each individual has

four covariates, namely treatment, thickness, age and sex. To illustrate the methodology we added 4000 dummy genes to this data set to give a data matrix with 4004 columns and 255 rows. By design the 4000 "genes" are not associated with survival time. Algorithmically, the challenge is to identify the important variables from 4004 potential predictors, most of which carry no information. The data were analysed using a parameteric Weibull model for the hazard function.

The algorithm selected only on variable: age. All of the pseudo gene variables were discarded rapidly. The Weibull shape parameter was estimates as 0.68.

Example 9: Ordered Categorical Analysis for prostate Cancer

The example is from Dhanasekaran et al 2001. See also http://www.nature.com/cgi-taf/DynaPage.taf?file=/nature/journal/v412/n6849/full/412822a0_fs.html

and the Supplementary files at

http://www.nature.com/nature/journal/v412/n6849/extref/412822aa.html

There are 15 samples (individuals) with 9605 genes. Missing values were replaced by row means + column means minus the grand mean. There were four ordered categories (G=4) namely

1. NAP normal
2. BPH benign
3. PCA localised
4. MET metastasised

The algorithm found 1 gene (gene number 6611, their accession ID R31679) which could correctly classify all the individuals apart from 1 misclassification.

The iterations from the EM algorithm are as follows:

```
************************************************
Iteration 1  :  10 cycles, criterion -6.346001
misclassification matrix
   fhat
f    1  2
  1 23  0
  2  0 22
row =true class
Class 1 Number of basis functions in model : 9608

************************************************
Iteration 2  :  5 cycles, criterion -13.21228
misclassification matrix
   fhat
f    1  2
  1 22  1
  2  1 21
row =true class
Class 1 Number of basis functions in model : 6127
************************************************
Iteration 3  :  4 cycles, criterion -14.11706
misclassification matrix
   fhat
f    1  2
  1 22  1
  2  2 20
row =true class
Class 1 Number of basis functions in model : 359
************************************************
```

```
Iteration 4   :  4 cycles, criterion -12.14269
misclassification matrix
   fhat
f     1   2
  1  23   0
  2   2  20
row =true class
Class 1 Number of basis functions in model : 44




************************************************
Iteration 5   :  5 cycles, criterion -9.134629
misclassification matrix
   fhat
f     1   2
  1  23   0
  2   1  21
row =true class
Class 1 Number of basis functions in model : 18
************************************************
Iteration 6   :  5 cycles, criterion -6.549706
misclassification matrix
   fhat
f     1   2
  1  23   0
  2   1  21
row =true class
Class 1 Number of basis functions in model :
************************************************
Iteration 7   :  5 cycles, criterion -4.988667
misclassification matrix
   fhat
```

```
f    1  2
  1 23  0
  2  1 21
row =true class
Class  1 : Variables left in model
1 2 3 408 6614 7191 8077
regression coefficients
16.0404 8.799716 4.196934 -0.004482982 -9.059594
0.01061934 -1.245061e-09
************************************************
Iteration 8  :  5 cycles, criterion -4.278911
misclassification matrix
   fhat
f    1  2
  1 23  0
  2  1 21
row =true class
Class  1 : Variables left in model
1 2 3 408 6614 7191
regression coefficients
20.00335 10.90405 5.268265 -1.996441e-05 -11.30149
0.001403909

************************************************
Iteration 9  :  4 cycles, criterion -3.980305
misclassification matrix
   fhat
f    1  2
  1 23  0
  2  1 21
row =true class
Class  1 : Variables left in model
1 2 3 408 6614 7191
regression coefficients
```

```
22.18902 12.03594 5.834313 -3.711782e-10 -12.53288
2.460434e-05


************************************************
Iteration 10  :  4 cycles, criterion -3.860487
misclassification matrix
   fhat
f    1  2
  1 23  0
  2  1 21
row =true class
Class  1 : Variables left in model
1 2 3 6614 7191
regression coefficients
23.18785 12.54724 6.089298 -13.09617 7.553351e-09
************************************************
Iteration 11  :  4 cycles, criterion -3.813712
misclassification matrix
   fhat
f    1  2
  1 23  0
  2  1 21
row =true class
Class  1 : Variables left in model
1 2 3 6614
regression coefficients
23.60507 12.76061 6.1956 -13.33150


************************************************
Iteration 12  :  3 cycles, criterion -3.795452
misclassification matrix
   fhat
```

```
f    1  2
  1 23  0
  2  1 21
row =true class
Class  1 : Variables left in model
1 2 3 6614
regression coefficients
23.7726 12.84627 6.238258 -13.42600
**********************************************
Iteration 13  :  3 cycles, criterion -3.788319
misclassification matrix
   fhat
f    1  2
  1 23  0
  2  1 21
row =true class
Class  1 : Variables left in model
1 2 3 6614
regression coefficients
23.83879 12.88010 6.255108 -13.46334


**********************************************
Iteration 14  :  3 cycles, criterion -3.785531
misclassification matrix
   fhat
f    1  2
  1 23  0
  2  1 21
row =true class
Class  1 : Variables left in model
1 2 3 6614
regression coefficients
23.86477 12.89339 6.261721 -13.47800
```

```
************************************************
Iteration 15  :  3 cycles, criterion -3.784442
misclassification matrix
   fhat
f    1  2
  1 23  0
  2  1 21
row =true class
Class  1 : Variables left in model
1 2 3 6614
regression coefficients
23.87494 12.89859 6.26431 -13.48373

************************************************
Iteration 16  :  2 cycles, criterion -3.784016
misclassification matrix
   fhat
f    1  2
  1 23  0
  2  1 21
row =true class
Class  1 : Variables left in model
1 2 3 6614
regression coefficients
23.87892 12.90062 6.265323 -13.48598
************************************************
Iteration 17  :  2 cycles, criterion -3.783849
misclassification matrix
   fhat
f    1  2
  1 23  0
  2  1 21
row =true class
Class  1 : Variables left in model
```

```
1 2 3 6614
regression coefficients
23.88047 12.90142 6.265719 -13.48686

**********************************************
Iteration 18  :  2 cycles, criterion -3.783784
misclassification matrix
   fhat
f     1  2
  1 23  0
  2  1 21
row =true class
Class  1 : Variables left in model
1 2 3 6614
regression coefficients
23.88108 12.90173 6.265874 -13.48720
```

Final misclassification table

```
   pred
y    1 2 3 4
  1  4 0 0 0
  2  0 2 1 0
  3  0 0 4 0
  4  0 0 0 4
Identifiers of variables left in ordered categories model
6611
Estimated theta
 23.881082 12.901727  6.265874
Estimated beta
 -13.48720
```

A plot of the fitted probabilities is given in Figure 6 below. The lines denote classes as follows: dashed line =class1 , solid line = class 2, dotted line = class 3, dotted and dashed line = class 4. Observations (index) 1

to 3 were in class 2, 4 to 7 were in class 1, 8 - 11 were in class 3 and 12 to 15 were in class 4.

Example 10: Ordered Categorical Analysis for prostate Cancer - Selected Genes

This example is identical to that of Example 9, with the exception that the data set has been reduced to 50 selected genes. One of these genes is the gene found significant in example 9, the others were selected at random. The purpose of this example is to provide an illustration based on a completely tabulated data set (Table 10).

Missing values were replaced by row means + column means minus the grand mean. There were four ordered categories (G=4) namely

1. NAP normal
2. BPH benign
3. PCA localized
4. MET metastasised

The algorithm found one predictive gene (gene 1 of table 10), which was equivalent to gene 6611 (Accession R31679) of Example 9. The prediction success was, of course, identical to that of example 9 (since it was based upon the same single gene).

Table 10: Disease Stage and Gene Expression for Selected Genes

	Disease Stage														
Gene	2	2	2	1	1	1	1	3	3	3	3	4	4	4	4
1	1.6520	1.1480	0.8600	2.2490	3.0190	4.0320	1.8900	0.9430	0.8890	0.7960	0.6340	0.1040	0.2040	0.2740	0.0830
2	1.0464	1.7040	1.0655	1.0860	1.0133	1.0509	1.0006	1.0568	1.0286	1.1060	0.9700	1.1016	0.6020	0.8080	1.0843
3	1.2402	1.2304	1.2594	0.9830	1.0700	1.2447	1.1945	1.2507	1.2225	0.4030	1.2067	1.2954	1.6620	1.8870	1.4340
4	0.4990	0.7100	0.7230	0.6700	0.7190	0.5520	0.9630	1.6230	1.0120	0.8945	1.2380	0.6350	0.8170	0.7040	1.4860
5	1.4324	1.1230	1.4516	1.1350	1.5340	1.3290	1.3867	2.3590	1.6770	1.2430	1.2450	1.4620	1.3950	1.3510	1.3320
6	0.9800	0.9580	1.0100	1.1800	1.0360	1.0610	1.3030	0.6610	0.9913	1.0209	1.1540	1.0643	0.7440	1.0190	1.0470
7	1.7784	1.9060	1.7976	0.8400	1.0520	1.4500	1.0560	4.7570	2.0600	1.2960	1.0810	1.4070	1.4900	1.7884	2.9420
8	0.8440	1.0800	1.1070	0.6570	1.0240	0.7510	1.1790	1.1830	1.0329	1.3040	1.1200	0.8010	1.3110	0.9640	1.3790
9	1.3625	1.6750	1.4220	0.9400	0.9850	1.8830	1.3168	1.3730	1.3448	1.3744	1.3290	1.4177	1.5270	1.3724	1.1030
10	0.7741	0.7850	0.5550	0.8690	0.6110	0.5410	0.7530	0.8450	0.9940	0.9300	0.9460	0.5900	0.7190	0.7030	0.9920
11	1.1284	1.1185	1.1475	1.0953	1.0953	1.1329	1.0826	1.1388	1.1106	1.1402	1.0949	1.1836	1.1541	1.1383	1.1280
12	0.8580	1.1825	1.0500	1.4560	1.0630	0.8470	1.0810	2.8890	1.1550	1.2042	1.0490	1.0310	0.9940	1.2023	0.8310
13	0.9030	0.9600	0.7650	1.2030	0.9290	1.2830	0.9800	0.9923	1.0480	0.8100	1.0060	0.9370	0.9120	0.9870	1.0170
14	1.7000	2.0640	1.9900	2.1290	1.8380	1.9030	1.6590	1.8620	1.5200	2.0130	1.2440	1.2500	0.9360	2.2600	0.8790
15	0.8690	0.7930	0.8210	1.0060	0.8310	0.8410	0.8250	0.8290	0.8643	0.9080	0.8250	0.9373	0.7280	0.8920	1.3040
16	0.9720	1.0620	1.1040	0.8750	1.0280	0.9890	0.9260	0.8670	1.1260	1.2760	0.9860	0.8640	1.3490	1.5980	1.5790
17	0.9820	1.8410	1.0790	2.4510	0.9130	1.5380	0.9790	0.8130	0.8750	1.1919	1.1465	0.9150	1.2058	1.1899	0.5900
18	0.5040	0.7860	0.6460	0.7280	0.8910	0.6320	0.8390	0.4910	1.0340	0.6880	0.6200	0.3890	0.4400	0.6110	0.4640
19	1.1427	1.2020	1.3440	1.0730	1.1840	1.1472	1.0970	1.1532	1.1250	1.1546	1.1092	1.1979	1.1685	1.1160	0.9350
20	1.2235	1.2136	0.5470	1.1904	0.5230	0.5400	1.0620	1.2339	1.2057	0.6590	0.6020	5.0830	0.8880	1.2820	1.0450
21	0.4920	0.7360	0.6500	0.6520	0.5910	0.5610	0.7050	0.6170	0.6860	0.7080	0.7410	0.5170	0.9250	1.0530	1.6110
22	1.0880	0.7180	0.8170	0.9870	0.6760	1.2960	0.7440	0.5040	0.7100	0.5290	0.6840	0.5970	0.4910	0.5040	0.4740
23	0.8035	0.6580	0.8226	0.7705	0.5800	0.7730	0.7578	0.8140	0.7858	0.6750	0.7770	0.8587	0.8430	0.9720	1.1470
24	2.1321	2.4360	2.7240	1.6260	2.2290	2.7950	2.0864	2.7400	2.2740	2.1490	1.3600	3.0110	1.4560	1.0680	1.8450
25	0.8875	0.7710	0.8860	0.7840	0.9430	0.7260	0.9860	0.8980	0.8698	0.9440	0.7230	0.9428	1.1010	0.8320	1.0630
26	1.0330	1.0140	1.0050	1.0330	0.9580	1.1380	0.8830	0.7020	0.8170	0.8365	0.7400	0.6160	0.4830	0.5420	0.5750
27	0.8324	0.8225	0.8515	0.7993	0.7993	0.8369	0.8470	0.8428	0.8146	0.2880	0.7989	0.8876	0.8581	1.3610	0.8703
28	0.6400	0.8610	0.7840	0.9300	0.7740	0.7460	0.8090	0.8980	0.9080	0.7800	0.8180	1.3400	0.9380	0.8500	0.9690
29	1.1340	0.8940	0.9030	0.9320	0.9130	0.9630	0.9370	1.0760	1.0020	0.7160	0.9970	0.8790	0.8980	0.9820	1.4650
30	0.7230	0.6410	0.4990	0.7190	0.6390	0.5680	0.6970	0.7320	0.6130	0.5620	0.8380	0.7782	0.7340	0.9250	1.2270
31	1.6570	1.0600	1.4730	1.1390	1.3130	1.2250	1.0770	0.7370	0.8930	0.9840	0.8300	1.1270	0.6860	0.9930	0.5080
32	0.5460	0.5370	0.4830	0.8570	0.5820	0.5560	0.7520	0.6900	0.8480	0.7360	0.6210	0.6410	0.7410	0.6990	1.2750
33	0.8792	0.6450	0.5600	0.9270	0.7950	1.1120	0.8335	0.8897	0.8615	0.8911	0.8070	0.9345	0.9170	1.1900	0.9570

	Disease Stage														
Gene	2	2	2	1	1	1	1	3	3	3	3	4	4	4	4
34	0.8244	0.6000	1.1050	0.9200	0.9440	0.8289	0.9430	0.8020	0.8067	0.7580	0.6690	0.8797	0.9030	0.5890	0.8320
35	0.9160	0.7790	0.7770	1.2340	0.7430	1.1970	0.7860	0.6580	0.8250	0.3920	0.5450	0.8440	0.5240	0.6310	0.7320
36	0.8912	0.5390	0.7970	1.1880	0.6820	0.7010	0.8760	0.9970	0.8000	0.9060	0.8980	1.1740	1.0260	0.7550	1.1330
37	1.1840	1.2700	1.4890	0.8670	1.2400	1.2230	1.0870	1.2670	1.3870	1.9100	1.2300	1.2190	1.2703	0.8150	1.2300
38	1.1304	1.1205	1.1495	1.0973	1.0973	1.5090	0.6400	1.1408	1.1126	1.1422	1.0969	1.1856	1.1561	1.1403	1.2410
39	1.4857	2.0350	1.5048	1.1970	1.9620	1.5820	1.7220	1.9630	1.4430	1.8120	1.9020	1.2850	0.8840	0.9620	0.5600
40	1.9650	1.6730	1.7710	1.4780	1.3830	1.7990	1.0340	0.7250	0.7970	0.7560	1.0390	0.4410	0.4940	0.7770	0.4780
41	0.8110	0.9690	1.0640	1.0330	0.7280	0.7810	0.8790	0.9281	0.7830	0.9610	1.1140	1.2200	0.7270	0.9320	0.8390
42	1.5686	2.6710	2.6750	1.3670	1.2040	1.7650	1.4580	1.5791	1.0230	1.5810	2.0400	1.8630	1.0030	1.1640	0.5730
43	0.9814	0.9715	1.0005	0.9483	0.9483	0.9859	0.9810	0.9918	0.9636	0.9932	0.9479	1.0366	1.0071	0.9913	1.0193
44	1.1596	1.7120	1.1760	1.1980	1.3410	1.0080	1.1139	1.2340	1.1419	1.1715	1.1262	0.8310	1.1854	1.1695	0.7740
45	0.9870	1.1340	1.2600	0.8850	1.0880	0.8450	1.0060	0.9790	1.0850	1.1040	1.2680	2.4300	0.9370	0.8080	0.9910
46	1.1520	1.0002	0.9720	0.7860	1.1950	0.9610	1.0550	0.9800	0.9923	0.8080	1.0300	1.0653	1.0410	1.2110	0.9250
47	0.9300	0.9154	0.8450	0.5610	0.8790	0.7310	0.8796	0.7120	0.9076	1.0470	0.9990	0.9805	0.9450	1.2500	1.2750
48	0.5700	0.7360	0.5800	0.7800	0.5720	0.8418	0.6720	0.6990	0.8196	0.8960	0.8450	0.8570	1.2200	1.2220	1.2310
49	1.4900	1.3340	0.9800	1.1665	1.0320	1.2690	1.1310	1.2100	1.1818	1.2114	1.0980	1.3380	1.3520	1.1020	1.0650
50	1.4590	1.2200	1.4490	1.7810	1.7520	1.3200	1.2210	1.0720	1.1140	1.4820	1.1160	0.5410	0.4620	0.4840	0.4910

Table E4: Disease Stage and Gene Expression for Selected Gene

EXAMPLE 11 Apparatus for use of the method.

Referring to Figure 5, a personal computer 20 suitable for implementing methods according to embodiments of the present invention is shown. Computer 20 operates under the instruction of a software program stored on hard disk data storage device 21. Computer 20 further includes a processor 22, memory 23, display screen 24, printer 25 and input devices mouse 26 and keyboard 27. The computer may have communication means such as a network connection 27 to the internet 28 or data collecting means 28 to facilitate downloading or collection and sharing of data.

The data collection means collects or downloads data from a system. The computer includes a manipulation means embodied in software which communicates with mouse 26 and keyboard 27 to allow a user to implement the method according to the embodiments of the invention on the data. The systems includes a means embodied in the software to implement the method according to the embodiments of the present invention, and means to create a graphic. After the method has been implemented, the output may be illustrated graphically on display screen 24 and/or printed on printer 25.

In the above examples, implementation of the invention has been described in relation to a biological system. As discussed previously, the invention may be applied to any "system" requiring features of samples to be predicted. Examples of systems include chemical systems, agricultural systems, weather systems, financial systems including, for example, credit risk assessment systems, insurance systems, marketing systems or company record systems, electronic systems, physical systems, astrophysics systems and mechanical systems.

Modifications and variations as would be apparent to a skilled addressee are deemed to be within the scope of the present invention.

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CLAIMS

1. A method for identifying a subset of components of a system, the subset being capable of predicting a feature of a test sample, the method comprising the steps of;

(a) generating a linear combination of components and component weights in which values for each component are introduced from data generated from a plurality of training samples, each training sample having a known feature;

(b) Defining a model for the probability distribution of a feature wherein the model is conditional on the linear combination and wherein the model is not a combination of a binomial distribution for a two class response with a probit function linking the linear combination and the expectation of the response;

(c) constructing a prior distribution for the component weights of the linear combination comprising a hyperprior having a high probability density close to zero;

(d) combining the prior distribution and the model to generate a posterior distribution;

(e) identifying a subset of components having component weights that maximise the posterior distribution.

2. The method of claim 1 wherein the model is a likelihood function based on a model selected from the group comprising a multinomial or binomial logistic regression, generalised linear model, Cox's proportional hazards model and parametric survival model.

3. The method of claim 1 or 2 wherein the model is a likelihood function based on a multinomial or binomial

logistic regression.

4. The method of claims 2 or 3 wherein the logistic regression models a feature having a multinomial or binomial distribution.

5. The method of any one of claims 1 to 4 wherein the subset of components is capable of classifying a sample into one of a plurality of pre-defined groups by defining a logistic regression which comprises grouping the samples into a plurality of sample groups, each sample group having a common group identifier.

6. The method of any one of claims 1 to 5 wherein the logistic regression is of the form:

$$L = \prod_{i=1}^{n} \left(\prod_{g=1}^{G-1} \left\{ \frac{e^{x_i^T \beta_g}}{\left(1 + \sum_{g=1}^{G-1} e^{x_i^T \beta_g} \right)} \right\}^{e_{ig}} \left\{ \frac{1}{1 + \sum_{h=1}^{G-1} e^{x_i^T \beta_h}} \right\}^{e_{iG}} \right)$$

wherein

$x_i^T \beta_g$ is a linear combination generated from input data from training sample i with component weights β_g;

x_i^T is the components for the i^{th} Row of X and β_g is a set of component weights for sample class g;

e_{ig} =1 if training sample i is a member of class g, e_{ig} =0 otherwise;

and

X is data from n training samples comprising p components.

7. The method of claim 1 or 2 wherein the subset of components is capable of classifying a sample into a

class wherein the class is one of a plurality of predefined ordered classes, by defining a logistic regression which comprises defining a series of group identifiers in which each group identifier corresponds to a member of an ordered class, and grouping the samples into one of the ordered classes.

8. The method of claim 7 wherein the logistic regression is of the form:

$$L = \prod_{i=1}^{N} \prod_{k=1}^{G-1} \left(\frac{\gamma_{ik}}{\gamma_{ik+1}} \right)^{r_{ik}} \left(\frac{\gamma_{ik+1} - \gamma_{ik}}{\gamma_{ik+1}} \right)^{r_{ik+1} - r_{ik}}$$

$$\operatorname{logit}\left(\frac{\gamma_{ik+1} - \gamma_{ik}}{\gamma_{ik+1}} \right) = \operatorname{logit}\left(\frac{\pi_{ik}}{\gamma_{ik+1}} \right) = \theta_k + x_i^T \beta^*$$

Wherein

$\square_{ik}$ is the probability that training sample i belongs to a class with identifier less than or equal to k (where the total of ordered classes is G);

$x_i^T \square^{\square}$ is a linear combination generated from input data from training sample i with component weights $\square^{\square}$;

X is data from n training samples comprising p components;

x_i^T is the components for the i^{th} Row of X ;

r_{ij} is as defined as

$$r_{ij} = \sum_{g=1}^{j} c_{ig}$$

where

$$c_{ij} = \begin{cases} 1, & \text{if observation i in class j} \\ 0, & \text{otherwise} \end{cases}$$

9. The method of claim 1 or 2 wherein the model is a likelihood function is based on a generalised linear model.

10. The method of claim 9 wherein the generalised linear model models a feature that is distributed as a regular exponential family of distributions.

11. The method of claim 10 wherein the regular exponential family of distributions is selected from the group consisting of normal distribution, Gaussian distribution, Poisson distribution, exponential distribution, gamma distribution, Chi Square distribution and inverse gamma distribution.

12. The method of claim 1 or 2 wherein the subset of components is capable of predicting a predefined characteristic of a sample by defining a generalised linear model which comprises modelling the characteristic to be predicted.

13. The method of claims 9 or 10 wherein the generalised linear model is of the form:

$$\log p(y \mid \beta, \varphi) = \sum_{i=1}^{N} \{ \frac{y_i \theta_i - b(\theta_i)}{a_i(\varphi)} + c(y_i, \varphi) \}$$

Wherein

$y = (y_1, \ldots, y_n)^T$, and y_i is the characteristic measured on the i^{th} sample;

$a_i(\phi) = \phi / w_i$ with the w_i being a fixed set of known weights and ϕ a single scale parameter;

the functions b(.) and c(.)are as defined by Nelder and Wedderburn (1972);

$E\{y_i\} = b'(\theta_i)$

$Var\{y\} = b''(\theta_i)a_i(\varphi) = \tau_i^2 a_i(\varphi)$;

and wherein each observation has a set of covariates x_i and a linear predictor $\eta_i = x_i^T \beta$.

14. The method of claim 1 or 2 wherein the model is a likelihood function based on a model selected from the group consisting of Cox's proportional hazards model, parametric survival model and accelerated survival times model.

15. The method of claim 1 wherein the subset of components is capable of predicting the time to an event for a sample by defining a likelihood based on Cox's proportional standards model, a parametric survival model or an accelerated survival times model, which comprises measuring the time elapsed for a plurality of samples from the time the sample is obtained to the time of the event.

16. The method of claim 14 wherein Cox's proportional hazards model is of the form:

$$L\left(\underset{\sim}{t} \mid \underset{\sim}{\beta}\right) = \prod_{j=1}^{N} \left(\frac{exp\left(Z_j \underset{\sim}{\beta}\right)}{\sum_{i \in \Re_j} exp\left(Z_i \underset{\sim}{\beta}\right)} \right)^{d_j}$$

Wherein

X is data from n training samples comprising p components;

Z is a matrix that is the re-arrangement of the rows of X where the ordering of the rows of Z corresponds to the ordering induced by the ordering of the survival times;

d is the result of ordering the censoring index with the same permutation required to order survival times.

Z_j is the j^{th} row of the matrix Z and d_j is the j^{th} element of d;

$\underset{\sim}{\beta}^T = (\beta_1, \beta_2, \cdots, \beta_p)$;

$\Re_j = \{i : i = j, j+1, \cdots, N\}$ = the risk set at the j^{th} ordered event time $t_{(j)}$;

17. The method of claim 14 wherein the parametric hazards model is of the form:

$$log(L) = \sum_{i=1}^{N} \left\{ c_i \log(\mu_i) - \mu_i + c_i \left(log\left(\frac{\lambda(y_i)}{\Lambda(y_i; \underset{\sim}{\varphi})} \right) \right) \right\}$$

where

$\mu_i = \Lambda(y_i; \underset{\sim}{\varphi}) exp(X_i \underset{\sim}{\beta})$;

$c_i = 1$ if the i^{th} sample is uncensored and $c_i = 0$ if the i^{th} sample is uncensored;

The functions $\lambda(.)$ and $\Lambda(.)$ are as defined by Aitkin and Clayton (1980);

X_i is the i^{th} row of X and X is data from n training samples comprising p components;

18. The method of any one of claims 1 to 17 wherein the prior distribution is of the form:

$$p(\beta) = \int_{\nu^2} p(\beta|\nu^2)\, p(\nu^2)\, d\nu^2$$

Where $p(\beta|\nu^2)$ is $N(0, \mathrm{diag}\{\nu^2\})$;

ν is a hyper parameter;

$p(\nu^2)$ is a hyperprior distribution.

19. The method of any one of claims 1 to 18 wherein the hyperprior is a Jeffreys prior of the form:

$$p(\nu^2) \alpha \prod_{i=1}^{n} 1/\nu^2$$

20. The method of any one of claims 1 to 19 wherein posterior distribution is of the form:

$$p(\beta \varphi \nu | y) \alpha L(y|\beta\varphi)\, p(\beta|\nu^2)\, p(\nu^2)$$

wherein $L(\underset{\sim}{y}|\underset{\sim}{\beta},\underset{\sim}{\varphi})$ is the likelihood function.

21. The method of any one of claims 1 to 20 wherein the posterior distribution is maximised using an iterative procedure.

22. The method of claim 21 wherein the iterative procedure is an EM algorithm.

23. The method of any one of claims 1 to 22 wherein the system is a biological system.

24. The method of claim 23 wherein the biological system is a biotechnology array.

25. The method of claim 24 wherein the biotechnology array is selected from the group consisting of DNA array,

protein array, antibody array, RNA array, carbohydrate array, chemical array, lipid array.

26. A method for identifying a subset of components of a subject which are capable of classifying the subject into one of a plurality of predefined groups wherein each group is defined by a response to a test treatment comprising the steps of:

(d) exposing a plurality of subjects to the test treatment and grouping the subjects into response groups based on responses to the treatment;
(e) measuring components of the subjects;
(f) identifying a subset of components that is capable of classifying the subjects into response groups using the methods according to any one of claims 1 to 28.

27. The method of claim 26 wherein the components are selected from the group consisting of genes, small nucleotide polymorphisms (SNPs), proteins, antibodies, carbohydrates, lipids.

28. An apparatus for identifying a subset of components of a system from data generated from the system from a plurality of samples from the system, the subset being capable of predicting a feature of a test sample, the apparatus comprising;

(a) means for generating a linear combination of components and component weights in which values for each component are introduced from data generated from a plurality of training samples, each training sample having a known feature;
(b) means for defining a model for the probability distribution of a feature wherein the model is conditional on the linear combination and wherein the

model is not a combination of a binomial distribution for a two class response with a probit function linking the linear combination and the expectation of the response;

(c) means for constructing a prior distribution for the component weights of the linear combination comprising a hyperprior having a high probability density close to zero;

(d) means for combining the prior distribution and the model to generate a posterior distribution;

(e) means for identifying a subset of components having component weights that maximise the posterior distribution.

29. A computer program arranged, when loaded onto a computing apparatus, to control the computing apparatus to implement a method in accordance with any one of claims 1 to 27.

30. The computer program of claim 29 implemented with the method of any one of claims 1 to 27.

31. A computer readable medium providing a computer program in accordance with claim 29 or 30.

32. A method of testing a sample from a system to identify a feature of the sample, the method comprising the steps of testing for a subset of components which is diagnostic of the feature, the subset of components having been determined by a method in accordance with any one of claims 1 to 27.

33. An apparatus for testing a sample from a system to determine a feature of the sample, the apparatus including means for testing for components identified in accordance with the method of any one of claims 1 to 27.

34. A computer program which when run on a computing device, is arranged to control the computing device, in a method of identifying components from a system which are capable of predicting a feature of a test sample from the system, and wherein a linear combination of components and component weights is generated from data generated from a plurality of training samples, each training sample having a known feature, and a posterior distribution is generated by combining a prior distribution for the component weights comprising a hyperprior having a high probability distribution close to zero, and a model that is conditional on the linear combination wherein the model is not a combination of a binomial distribution for a two class response with a probit function linking the linear combination and the expectation of the response, to estimate component weights which maximise the posterior distribution.

35. A method for identifying a subset of components of a biological system, the subset being capable of predicting a feature of a test sample from the biological system, the method comprising the steps of:

(a) generating a linear combination of components and component weights in which values for each component are determined from data generated from a plurality of training samples, each training sample having a known feature;

(b) defining a model for the probability distribution of a feature wherein the model is conditional on the linear combination;

(c) constructing a prior distribution for the component weights of the linear combination comprising a

hyperprior having a high probability density close to zero;

(d) combining the prior distribution and the model to generate a posterior distribution;

(e) identifying a subset of components having component weights that maximise the posterior distribution.

FIGURE 1

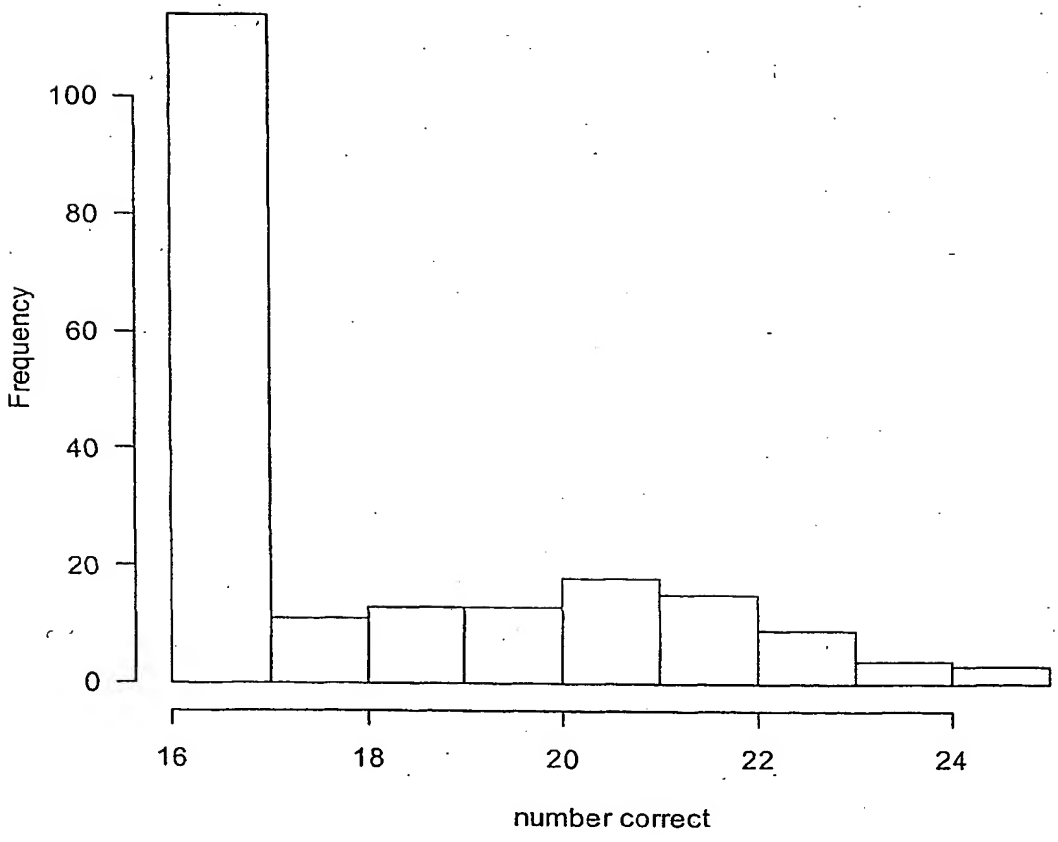


FIGURE 2

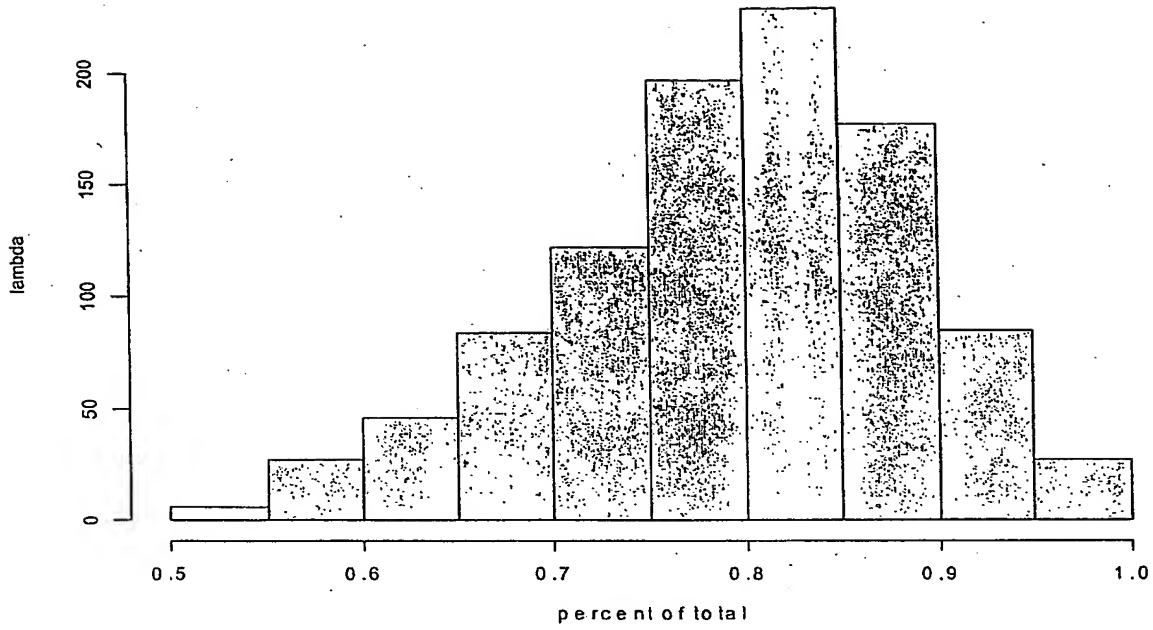


FIGURE 3

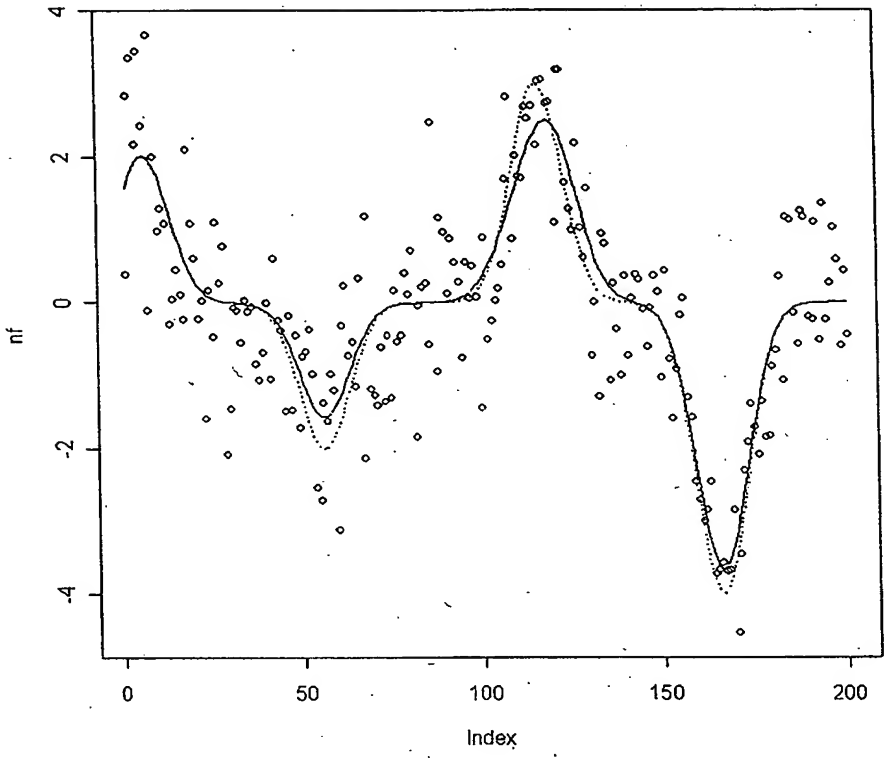


FIGURE 4

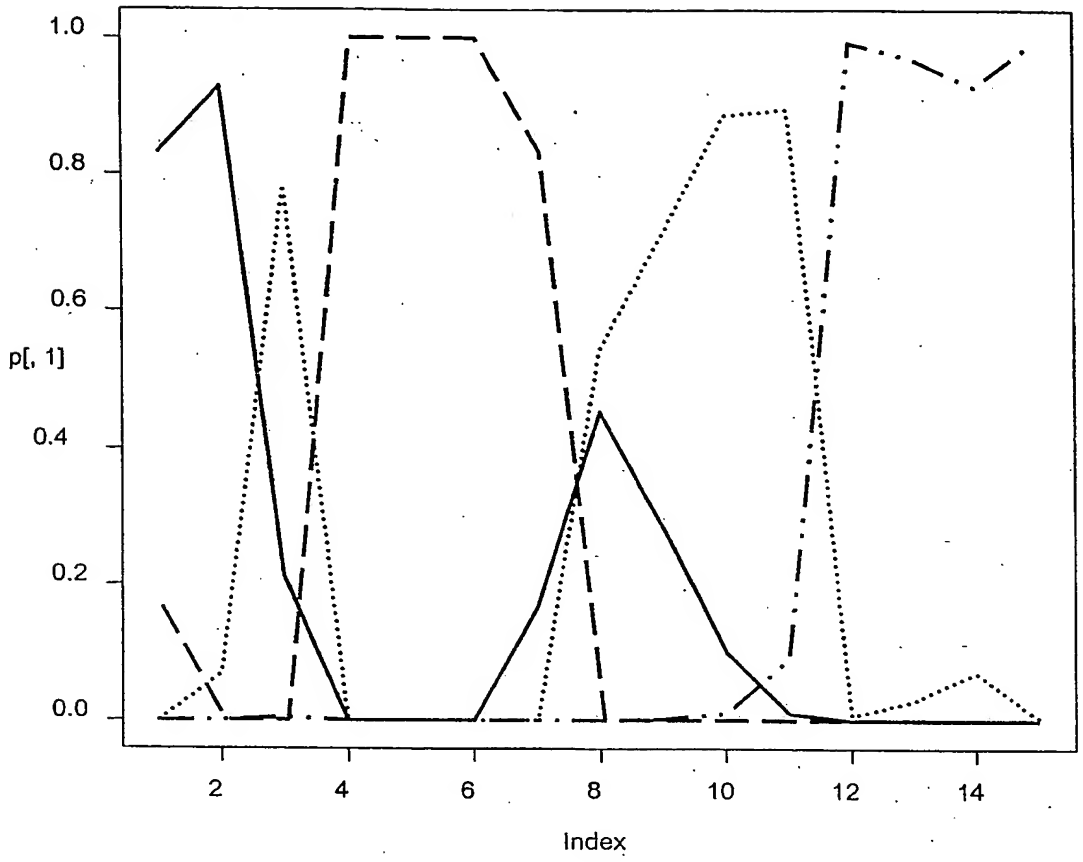
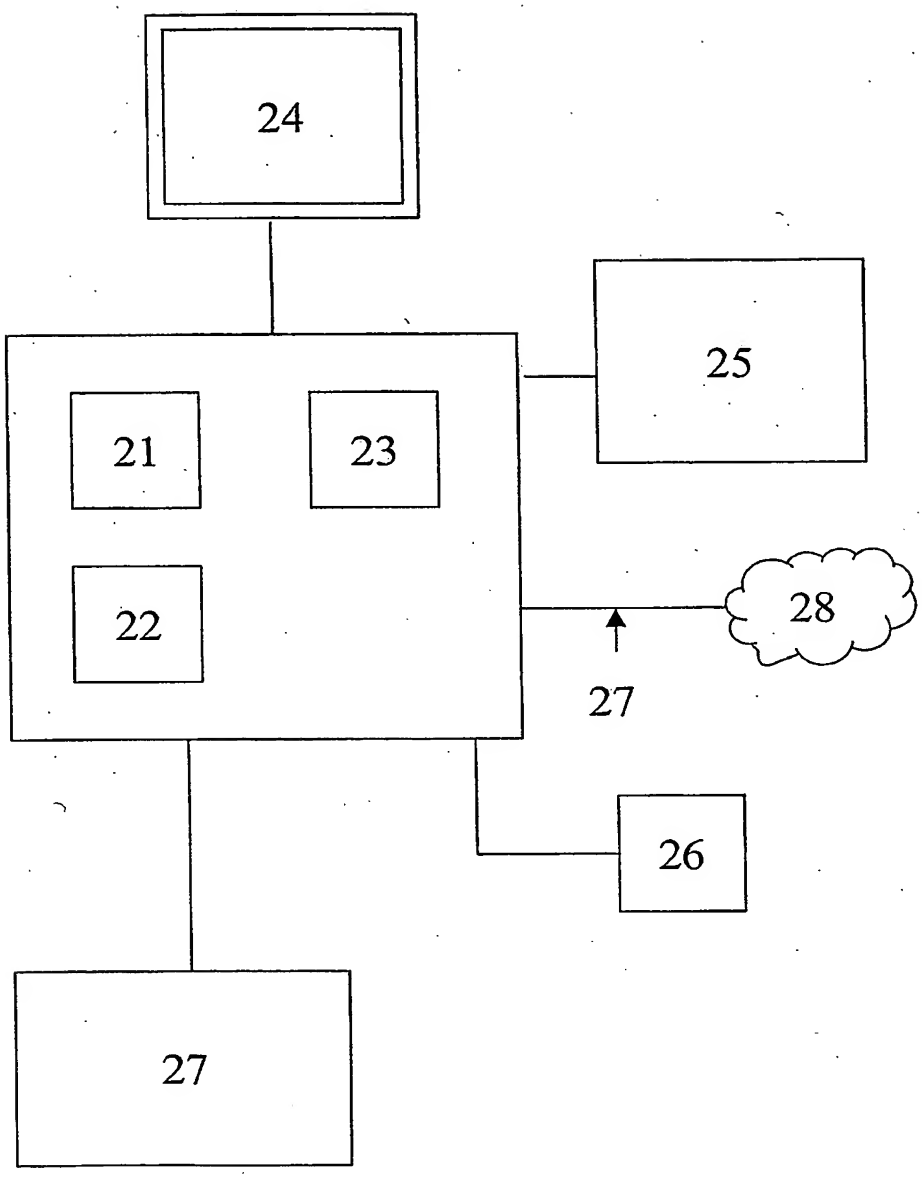


FIGURE 5



INTERNATIONAL SEARCH REPORT

International application No.
PCT/AU02/01417

A. CLASSIFICATION OF SUBJECT MATTER

Int. Cl. [7]: G06F 17/18, G06F 15/18

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
IPC:

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
WPAT, G06F 17/18 and Keywords (Bayesian, Posterior distribution, DNA and like terms)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
P, X	EP 1158436 (NCR International Inc.) 28 November 2001 Page 4 Line 14 onwards	1 to 35
A	WO 01/75639 (PHARMACIA & UPJOHN S.P.A) 11 October 2001	
A	US 5713016 (Hill) 27 January 1998	

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Date of the actual completion of the international search	Date of mailing of the international search report
6 November 2002	11 NOV 2002
Name and mailing address of the ISA/AU AUSTRALIAN PATENT OFFICE PO BOX 200, WODEN ACT 2606, AUSTRALIA E-mail address: pct@ipaustralia.gov.au Facsimile No. (02) 6285 3929	Authorized officer **J. THOMSON** Telephone No : (02) 6283 2214

INTERNATIONAL SEARCH REPORT

Information on patent family members

International application No.
PCT/AU02/01417

This Annex lists the known "A" publication level patent family members relating to the patent documents cited in the above-mentioned international search report. The Australian Patent Office is in no way liable for these particulars which are merely given for the purpose of information.

Patent Document Cited in Search Report		Patent Family Member			
US	5713016	NONE			
WO	200175639	AU	200154723		
EP	1158436	JP	2002056341	US	2002016699

END OF ANNEX

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